WEST Search History

DATE: Tuesday, October 22, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L24	L22 and cis	60	L24
L23	L22 and cis act$8	664146	L23
L22	L21 and display adj4 librar$4	100	L22
L21	(In adj4 vitro) adj5 (peptide or polypeptide or P2A)	670	L21
DB=USPT; PLUR=YES; OP=OR			
L20	L19 and cis adj4 act$8	5	L20
L19	L18 and in adj4 vitro	16986	L19
L18	libra$4 adj6 (peptide or polypeptide or protein) adj4 bind$6 adj 5 (DNA or gene or cDNA)	86711	L18
L17	L13 and covalent adj4 (DNA encod$5)	0	L17
L16	L10 and cis adj4 act$6	0	L16
L15	L10 and cis act$5	1978737	L15
L14	L10 and (DNA or cDNA or gene) adj4 encod$4	0	L14
L13	(L7 and covalent adj4 (DNA encod$5)) AnD ((@pd > 20021022)!)	0	L13
L12	(peptide or polypeptide or protein) adj4 libra$4	4021	L12
L11	L8 and DNA adj4 librar$4	6958	L11
L10	(L4 and cis adj4 act$6) AnD ((@pd > 20021022)!)	0	L10
L9	cis adj3 act$5 adj4 (protein or polypeptide or peptide)	73	L9
L8	cis adj3 act$5 adj 4(protein or polypeptide or peptide)	139317	L8
L7	(L4 and cis act$5) AnD ((@pd > 20021022)!)	0	L7
L6	(L4 and (DNA or cDNA or gene) adj4 encod$4) AnD ((@pd > 20021022)!)	0	L6
L5	((peptide or polypeptide or protein) adj4 libra$4) AnD ((@pd > 20021022)!)	0	L5
L4	(L2 and DNA adj4 librar$4) AnD ((@pd > 20021022)!)	0	L4
L3	(cis adj3 act$5 adj4 (protein or polypeptide or peptide)) AnD ((@pd > 20021022)!)	0	L3
L2	(cis adj3 act$5 adj 4(protein or polypeptide or peptide)) AnD ((@pd > 20021022)!)	0	L2
L1	((((peptide or polypeptide or protein) adj4 libra$4)and cis adj4 act$6) and covalent adj4 (DNA encod$5))	1	L1

END OF SEARCH HISTORY

translation termination codon within the 2Apro coding region. The reduced
expression from the 2Apro vector results from a 4-fold reduction in DNA replication and 22-fold reduction in transcription by RNA polymerase H from
the adenovirus major late promoter/SV40 enhancer utilized in this vector. In contrast, no decrease in transcription of the adenovirus virus-associated
I RNA gene by RNA polymerase III was observed The effect of 2Apro expression
on cap-dependent mRNA translation was studied by producing a dicistronic β-globin mRNA harboring the encephalomyocarditis virus leader and 2Apro-coding region within the 3' end of the mRNA to mediate cap-independent translation of 2Apro. Expression of this mRNA was also reduced 25-fold compared to an identical plasmid harboring a termination codon within the 2Apro coding region. Translation of the β-globin marker gene from this mRNA was reduced 3-fold when corrected for mRNA level.
These results suggest that p220 cleavage itself is not sufficient for complete inhibition of host translation and that an important effect of 2Apro expression on host protein synthesis is a reduction in RNA polymerase II
transcription and to a lesser extent, DNA replication. This reduction could
be a primary effect of 2Apro, or a secondary effect caused by the inhibition of translation.

L13 ANSWER 8 OF 8 CA COPYRIGHT 2002 ACS
TI The nucleotide sequence of the structural-protein-coding region of foot-and-mouth disease virus serotype SAT3
AU Brown, Alan L.; Campbell, Richard O.; Clarke, Berwyn E.
SO Gene (1989), 75(2), 225-34
CODEN: GENED6; ISSN: 0378-1119
PY 1989
AB The nucleotide sequence coding for the structural proteins and nonstructural protein P2A was determined for a foot-and-mouth disease virus
(FMDV) isolated in Africa. This virus, serotypically designated SAT3 (South African Territories type 3), shows ≈60% homol. at the nucleotide level to prototype viruses from the O, A, and C serotypes of FMDV. The highest region of variability was in structural protein VP1, presumably a consequence of its position on the surface of the virus and its exposure to selection pressure by neutralizing antibody. Within this region, amino acids (aa) 141-160, which have been shown to represent an immunodominant region in other FMDV serotypes, showed hypervariability as well as the insertion of 5 or 9 addnl. aa relative to the O1 and C1 serotypes, resp. In contrast, the sequence of nonstructural protein P2A was completely conserved, indicating a probable important role in virus replication.

=> d his

(FILE 'HOME' ENTERED AT 10:36:17 ON 22 OCT 2002)

FILE 'CA' ENTERED AT 10:36:27 ON 22 OCT 2002
L1 0 S IN VITRO DNA LIBR?
L2 46 S CIS(2W)ACT?(2W)(PEPTIDE OR POLYPEPTIDE OR PROTEIN)
L3 0 S L2 NOT 199-2002/PY
L4 40 S L2 NOT 1999-2002/PY

```
L5            1 S L4 AND DNA(2W)BIND?(2W)PROTEIN
L6           39 S L4 NOT L5
L7            1 S L6 AND LIBR?
L8           38 S L6 NOT L7
L9       501199 S IN VITRO
L10        4108 S L9 AND LIBRAR?
L11          61 S L10 AND DNA(2W)BIND?(4W)(PEPTIDE OR POLYPEPTIDE OR PROTEIN)
L12          44 S L11 NOT 1999-2002/PY
L13           8 S P2A (5W)(PEPTIDE OR POLYPEPTIDE OR PROTEIN)
```

```
=> s in vitro DNA libr?
        501199 VITRO
        560869 DNA
         72074 LIBR?
L1           0 IN VITRO DNA LIBR?
                 (VITRO(W)DNA(W)LIBR?)

=> s cis(2w)act?(2w)(peptide or polypeptide or protein)
        180062 CIS
       3947032 ACT?
        273170 PEPTIDE
         86631 POLYPEPTIDE
       1411336 PROTEIN
L2          46 CIS(2W)ACT?(2W)(PEPTIDE OR POLYPEPTIDE OR PROTEIN)

=> s l2 not 199-2002/py
      21179974 199-2002/PY
L3           0 L2 NOT 199-2002/PY

=> s l2 not 1999-2002/py
       2767092 1999-2002/PY
L4          40 L2 NOT 1999-2002/PY

=> s l4 and DNA(2w)bind?(2w)protein
        560869 DNA
        919423 BIND?
       1411336 PROTEIN
          7635 DNA(2W)BIND?(2W)PROTEIN
L5           1 L4 AND DNA(2W)BIND?(2W)PROTEIN

=> d l5 ti au so py ab

L5   ANSWER 1 OF 1  CA  COPYRIGHT 2002 ACS
TI   On the nature of cis-acting regulatory proteins and genetic organization
     in bacteriophage:  the example of gene Q of bacteriophage λ
AU   Echols, Harrison; Court, Donald; Green, Linda
SO   Genetics (1976), 83(1), 5-10
     CODEN: GENTAE
PY   1976
AB   A partially cis-acting regulatory protein
     was found in phage λ: the product of the phage Q gene.  There may
     be a complete spectrum from all-cis to all-trans for such regulatory
     proteins.  This behavior might arise because a DNA-
     binding protein either acts at a nearby cis site soon
     after synthesis or becomes lost for its trans activity on another genome
     through nonspecific interactions with DNA.  The proposed explanation
     provides one evolutionary basis for the linkage of genes for regulatory
     proteins and the sites at which such proteins act; it also suggests a
     possible rationale for the metabolic instability of certain regulatory
     proteins.


=> s l4 not l5
L6          39 L4 NOT L5

=> s l6 and libr?
         72074 LIBR?
L7           1 L6 AND LIBR?
```

=> d l7 ti au so py ab

L7 ANSWER 1 OF 1 CA COPYRIGHT 2002 ACS
TI Activation of junB by PKC and PKA signal transduction through a novel cis-acting element
AU De Groot, Rolf P.; Auwerx, Johan; Karperien, Marcel; Staels, Bart; Kruijer, Wiebe
SO Nucleic Acids Research (1991), 19(4), 775-81
CODEN: NARHAD; ISSN: 0305-1048
PY 1991
AB The product of the junB gene, a gene homologous to the proto-oncogene c-jun, is a component of transcription factor AP-1. JunB expression is modulated by a wide variety of extracellular stimuli, such as serum, growth factors, phorbol esters (TPA) and activators of protein kinase A (PKA). In order to study the mol. basis of this complex regulation, the mouse junB gene was cloned from a genomic testis **library**. The junB promoter was characterized. The junB promoter is activated by serum, TPA, and activated PKA. Sequences located between -91 and -44 are necessary for induction. These sequences contain a CAAT box, a G-C rich region and a previously undescribed inverted repeat (IR). The IR element can mediate induction by TPA and PKA when coupled to a heterologous promoter, and specifically binds a protein of 110 kD.

=> s l6 not l7
L8 38 L6 NOT L7

=> d l8 1-38 au so py ab

L8 ANSWER 1 OF 38 CA COPYRIGHT 2002 ACS
AU Kubota, Satoshi; Pomerantz, Roger J.
SO Oncogene (1998), 16(14), 1851-1861
CODEN: ONCNES; ISSN: 0950-9232
PY 1998
AB A peptide signal, which may control nucleo-cytoplasmic protein trafficking, was newly identified in human immunodeficiency virus type I (HIV-1) Rev, a lentiviral post-transcriptional transactivator. The sequence, in the amino-terminal portion of HIV-1 Rev, maintains a Rev mutant with a dysfunctional nuclear/nucleolar targeting signal outside of the nucleus, although this Rev mol. itself is small enough to pass through the nuclear pores. Transition of this sequence to the N-terminus of human T-lymphocytic leukemia/lymphoma virus type I (HTLV-I) p21x, which is usually located evenly distributed throughout the cell, resulted in capture of p21x in the cytoplasm. Mutational anal. clarified that a 14 residue peptide sequence was sufficient to display this inhibitory effect against nuclear entry. Furthermore, this HIV-1 Rev sequence was capable of inhibiting nuclear entry of a fragment of a human ribosomal protein, when it was fused to the carboxy terminus. The identified nuclear entry inhibitory signal (NIS) contains a conserved hydrophilicity motif, which forms an amphipathic helix. Significantly, this motif and its helical structure were shown to be important for NIS function and the HIV-1 Rev function itself. Possible roles for NIS as a mol. anchor are proposed herein.

L8 ANSWER 2 OF 38 CA COPYRIGHT 2002 ACS
AU Mori, Kazutoshi; Ogawa, Naoki; Kawahara, Tetsushi; Yanagi, Hideki; Yura, Takashi

SO Journal of Biological Chemistry (1998), 273(16), 9912-9920
CODEN: JBCHA3; ISSN: 0021-9258
PY 1998
AB When unfolded proteins are accumulated in the endoplasmic reticulum (ER), an intracellular signaling pathway termed the unfolded protein response (UPR) is activated to induce transcription of ER-localized mol. chaperones and folding enzymes in the nucleus. In Saccharomyces cerevisiae, at least six lumenal proteins including essential Kar2p and Pdi1p are known to be regulated by the UPR. We and others recently demonstrated that the basic-leucine zipper protein Hac1p/Ern4p functions as a trans-acting factor responsible for the UPR. Hac1p binds directly to the **cis -acting** unfolded **protein** response element (UPRE) responsible for Kar2p induction. Moreover, we showed that the KAR2 UPRE contains an E box-like palindrome separated by one nucleotide (CAGCGTG) that is essential for its function. We report here that the promoter regions of each of five target proteins (Kar2p, Pdi1p, Eug1p, Fkb2p, and Lhs1p) contain a single UPRE sequence that is necessary and sufficient for induction and that binds specifically to Hac1p in vitro. All of the five functional UPRE sequences identified contain a palindromic sequence that has, in four cases, a spacer of one C nucleotide. This unique characteristic of UPRE explains why only a specific set of proteins are induced in the UPR to cope with ER stress.

L8 ANSWER 3 OF 38 CA COPYRIGHT 2002 ACS
AU Camps, Montserrat; Chabert, Christian; Muda, Marco; Boschert, Ursula; Gillieron, Corine; Arkinstall, Steve
SO FEBS Letters (1998), 425(2), 271-276
CODEN: FEBLAL; ISSN: 0014-5793
PY 1998
AB In PC12 sympathetic neurons activation and nuclear translocation of ERK family MAP kinases plays an essential role in processes underlying nerve growth factor (NGF)-dependent differentiation. The authors have recently cloned MKP-3 as a novel dual specificity phosphatase displaying selectivity towards inactivation of the ERK1 and ERK2 MAP kinases. Here the authors report that in PC12 cells, MKP-3 undergoes powerful and specific up-regulation by NGF while a number of mitogens and cellular stresses are ineffective. NGF-stimulated MKP-3 expression appears after 1 h, is maximal at 3 h, and is sustained for 5 days. This coincides with a critical period of neurite outgrowth and terminal differentiation. Consistent with a role mediating inhibition of PC12 cell MAP kinases, NGF-stimulated ERK2 activation was suppressed considerably following pretreatment with fibroblast growth factor and 9-cis-retinal, two addnl. differentiation factors found to induce powerfully MKP-3 expression. Given the clear cytosolic localization of MKP3 in PC12 cells and sympathetic neurons, these results suggest a critical role for inactivating ERK MAP kinases in non-nuclear compartments during essential stages of NGF-mediated PC12 differentiation.

L8 ANSWER 4 OF 38 CA COPYRIGHT 2002 ACS
IN Mori, Kazutoshi; Kawahara, Tetsushi; Yanagi, Hideki; Yura, Takashi
SO Jpn. Kokai Tokkyo Koho, 21 pp.
CODEN: JKXXAF
PY 1998
AB The Saccharomyces cerevisiae gene ERN4 encoding 2 transcription factors Ern4p, that are resulted from differential splicing, is isolated and

characterized. The proteins are comprised of 230 and 238 amino acids, resp. The proteins specifically bind to the **cis-acting** unfolded **protein**-response element (UPRE) in vitro and activates transcription in vivo. Expression of the GAL4(ad)-ERN4 fusion gene constitutively induces the expression of Kar2p and Pdilp (stress response proteins) in Saccharomyces cerevisiae. Saccharomyces cerevisiae lacking Ern4p (mutant ern4δ) are unable to induce transcription of any of the five target genes tested and exhibit sensitivity to ER stress and inositol requirement for growth. The transcription factor can be used for the regulation of expression of heterologous proteins and stress response.

L8 ANSWER 5 OF 38 CA COPYRIGHT 2002 ACS
AU Lee, Jong-Soo; Lee, Chang-Hun; Chung, Jay H.
SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(3), 969-974
CODEN: PNASA6; ISSN: 0027-8424
PY 1998
AB Transcription is thought to be regulated by recruitment of transcription factors, adaptors, and certain enzymes to **cis-acting** elements through **protein**-DNA interactions and protein-protein interactions. To better understand transcription, a method with the capability to defect in vivo recruitment of these individual proteins will be essential. Toward this end, we use a previously undescribed in vivo method that we term protein position identification with nuclease tail (PIN*POINT). In this method, a fusion protein composed of a chosen protein linked to a nonsequence-specific nuclease is expressed in vivo, and the binding of the protein to DNA is made detectable by the nuclease-induced cleavage near the binding site. In this article, we used the technique protein position identification with nuclease tail to study the effect of the β-globin locus control region (LCR) and promoter elements on the recruitment of transcription factor Sp1 to the β-globin promoter. We present evidence that the hypersensitive sites of the LCR synergistically enhance the recruitment of a multimeric Sp1 complex to the β-globin promoter and that this may be accomplished by protein-protein interactions with proteins bound to the LCR, the upstream activator region, and, possibly, general transcription factors bound near the "TATA" box.

L8 ANSWER 6 OF 38 CA COPYRIGHT 2002 ACS
AU Gareus, Ralph; Gigler, Andreas; Hemauer, Andrea; Leruez-Ville, Marianne; Morinet, Frederic; Wolf, Hans; Modrow, Susanne
SO Journal of Virology (1998), 72(1), 609-616
CODEN: JOVIAM; ISSN: 0022-538X
PY 1998
AB Parvovirus B19 infections are associated with diverse clin. manifestations, ranging from no symptoms to severe symptoms. The virus shows an extreme tropism for replication in erythroid progenitor cells, possibly due to the activity of the only functional promoter (p6) of the B19 virus genome in combination with both cell- and cell cycle-specific factors and the trans-activator protein NS1. As presented here, p6 promoter sequences derived from several B19 virus isolates proved to be highly conserved. Furthermore, mutations did not affect any of the potential binding sites for transcription factors. One variation of the base at position 223 was identified only in B19 virus isolates derived from patients with

persistent infection or chronic arthritis. To determine promoter activity and to characterize regulatory elements, sequences spanning the total p6 promoter and subfragments of them were introduced into a eukaryotic expression vector upstream of the luciferase gene (from Photinus pyralis). After transfection into HeLa, CEM, BJAB, and K562 cells, the p6 promoter was found to be highly active. When introduced into the erythroid cell line K562, p6-controlled transcription exceeded that of the simian virus 40 promoter-enhancer used as a control by more than 25-fold. Sequence elements relevant for promoter activity mapped to the regions from nucleotides (nt) 100 to 190 and 233 to 298. Also, the segment from nt 343 to 400 downstream of the TATA box was important for transcriptional activity in HeLa and K562 cells. By transfecting the promoter-luciferase constructs into a HeLa cell line stably carrying the viral NS1 gene under the control of an inducible promoter, transcriptional activity mediated by the p6 promoter rose significantly after induction of NS1 expression. The region from nt 100 to 160 proved to be essential for NS1-mediated transcriptional activation. Furthermore, NS1-mediated transactivation was dependent on the presence of two GC-rich elements arranged in tandem upstream of the TATA box. These data indicate that NS1-mediated p6 transactivation is dependent on a multicomponent complex combining NS1 with ATF, NF-κB/c-Rel, and GC-box binding cellular factors.

L8 ANSWER 7 OF 38 CA COPYRIGHT 2002 ACS
AU Shen, Wen Hui; Gigot, Claude
SO Plant Molecular Biology (1997), 33(3), 367-379
CODEN: PMBIDB; ISSN: 0167-4412
PY 1997
AB The S phase-specific expression of histone genes provides an interesting model for studying activation of gene transcription during the cell cycle. In plants, however, trans-acting factors responsible for histone gene transcription are poorly documented. Using combined gel shift, UV crosslinking and competition anal., we carried out a systematic study to identify and characterize proteins binding with the previously established cis elements of the plant histone gene promoters. Nuclear exts. prepared from the highly synchronizable tobacco BY2 cells were used. We confirmed the presence of proteins binding to the hexamer (ACGTCA) motif which has been previously identified as the binding site of wheat HBP-1 proteins. Interestingly, multiple proteins were found to bind specifically with the nonamer (CAATCCAAC) element and their DNA-binding activity was abolished upon in vitro protein phosphatase treatment. This later result imply phosphorylation/dephosphorylation as a potential posttranslational control for DNA-binding activity of nonamer-binding proteins. In addition, the DNA-binding activity of these nonamer-binding proteins was found to be pos. correlated with the S phase-specific expression of the histone genes in the synchronized cells, suggesting their function in the activation of transcription during the G1/S transition. Finally, several proteins were observed to bind specifically with an A/T-rich hexamer (TAATAT) motif. Their DNA-binding activity, however, was insensitive to phosphatase activity in vitro and relatively constitutive during the cell cycle. This A/T-rich hexamer as a new cis-acting element of plant histone genes is discussed.

L8 ANSWER 8 OF 38 CA COPYRIGHT 2002 ACS
AU Mori, Kazutoshi; Kawahara, Tetsushi; Yoshida, Hiderou; Yanagi, Hideki; Yura, Takashi
SO Genes to Cells (1996), 1(9), 803-817
CODEN: GECEFL; ISSN: 1356-9597
PY 1996
AB Accumulation of unfolded proteins in the endoplasmic reticulum (ER) triggers the transcriptional induction of mol. chaperones and folding enzymes localized in the ER. Thus, eukaryotic cells possess an intracellular signalling pathway from the ER to the nucleus, called the unfolded protein-response (UPR) pathway. In Saccharomyces cerevisiae, such induction is mediated by the **cis-acting** unfolded **protein**-response element (UPRE) which has been thought to be recognized by one or more transcription factor(s). Extensive mutational anal. revealed that UPRE contains a partial palindrome with a spacer of one nucleotide (CAGCGTG) that is essential for its function. We then cloned the ERN4 (presumably identical with HAC1) gene using yeast one-hybrid screening, in which the GAL4-ERN4 fusion gene constitutively activates the UPR pathway. The ERN4 gene encodes a basic-leucine zipper protein (Ern4p) that specifically binds to UPRE in vitro and activates transcription in vivo. Cells lacking Ern4p are unable to induce transcription of any of the five target genes tested and exhibit sensitivity to ER stress and inositol requirement for growth. We concluded that Ern4p represents a major component of the putative transcription factor (UPRF) responsible for the UPR leading to the induction of ER-localized stress proteins.

L8 ANSWER 9 OF 38 CA COPYRIGHT 2002 ACS
AU Coyne, Robert S.; Chalker, Douglas L.; Yao, Meng Chao
SO Annual Review of Genetics (1996), 30, 557-578
CODEN: ARVGB7; ISSN: 0066-4197
PY 1996
AB A review with .apprx.112 refs. The ciliated protozoa divide the labor of germline and somatic genetic functions between two distinct nuclei. The development of the somatic (macro-) nucleus from the germinal (micro-) nucleus occurs during sexual reproduction and involves large-scale, genetic reorganization including site-specific chromosome breakage and DNA deletion. This intriguing process has been extensively studied in Tetrahymena thermophila. Characterization of **cis-acting** sequences, putative **protein** factors, and possible reaction intermediates has begun to shed light on the underlying mechanisms of genome rearrangement. This article summarizes the current understanding of this phenomenon and discusses its origin and biol. function. We postulate that ciliate nuclear restructuring serves to segregate the two essential functions of chromosomes: the transmission and expression of genetic information.

L8 ANSWER 10 OF 38 CA COPYRIGHT 2002 ACS
AU Spencer, Corinne Marie
SO (1995) 154 pp. Avail.: Univ. Microfilms Int., Order No. DA9615130
From: Diss. Abstr. Int., B 1996, 57(1), 142
PY 1995
AB Unavailable

L8 ANSWER 11 OF 38 CA COPYRIGHT 2002 ACS
AU Zanke, Brent W.; Boudreau, Kimberly; Rubie, Elizabeth; Winnett, Elaine; Tibbles, Lee Anne; Zon, Leonard; Kyriakis, John; Liu, Fei-Fei; Woodgett, James R.

SO Current Biology (1996), 6(5), 606-613
CODEN: CUBLE2; ISSN: 0960-9822
PY 1996
AB Stimuli that stress cells, including inflammatory cytokines, ultra-violet irradiation, DNA-damaging chemotherapeutic drugs and heat shock, stimulate a recently identified cytoplasmic signaling system that is structurally related to the mitogen-activated protein kinase pathway. This pathway consists of a cascade of protein kinases including stress-activated protein kinase (SAPK), also termed Jun N-terminal kinase (JNK), and two kinases that activate it, MEKK and SEK/MKK4. Despite rapid progress in delineating the components of this pathway, the cellular consequence of its activation remains to be defined. We have screened cells for defects in SAPK signaling and identified a cell line, previously characterized for its thermotolerance properties, as being more refractive to SAPK activation induced by heat stress than its thermosensitive parental line. Stable expression of dominant inhibiting SEK mutants in thermosensitive parental cells specifically and effectively blocked SAPK activation after heat shock. These lines also became markedly resistant to the cytocidal effects of thermal stress, confirming the phenotype of the thermotolerant line. These cell lines defective in SAPK activation were also resistant to the lethal effects of the DNA-damaging drug cis-platinum. Exptl. induced stable blockade of SAPK activation in cells with normal thermosensitivity is sufficient to confer resistance to cell death induced by diverse stimuli including heat and the chemotherapeutic agent cis-platinum. These results suggest that activation of the SAPK pathway by diverse cell stressors plays a critical part in mediating the toxicity of these treatments and inducing cell death. SAPK activation in this context could broadly influence cellular response to stress, modulate apoptosis during development or determine the clin. response of tumor cells to cytotoxic therapies.

L8 ANSWER 12 OF 38 CA COPYRIGHT 2002 ACS
AU Saleem, Ahamed; Datta, Rakesh; Yuan, Zhi-Min; Kharbanda, Surender; Kufe, Donald
SO Cell Growth & Differentiation (1995), 6(12), 1651-8
CODEN: CGDIE7; ISSN: 1044-9523
PY 1995
AB The cellular response to 1-β-D-arabinofuranosylcytosine (ara-C) includes activation of Jun/AP-1, induction of c-jun transcription, and programmed cell death. The stress-activated protein (SAP) kinases stimulate the transactivation function of c-jun by amino terminal phosphorylation. The present work demonstrates that ara-C activates p54 SAP kinase. The finding that SAP kinase is also activated by alkylating agents (mitomycin C and cis-platinum) and the topoisomerase I inhibitor 9-amino-camptothecin supports DNA damage as an initial signal in this cascade. The results demonstrate that ara-C also induces binding of SAP kinase to the SH2/SH3-containing adapter protein Grb2. SAP kinase binds to the SH3 domains of Grb2, while interaction of the p85 α-subunit of phosphatidylinositol 3-kinase (PI 3-kinase) with the Grb2 SH2 domain results in the formation of a SAP kinase/Grb2/PI 3-kinase complex. The results also demonstrate that ara-C treatment is associated within inhibition of lipid and serine kinase activities of PI 3-kinase. The potential

significance of the ara-C-induced interaction between SAP kinase and PI 3-kinase is further supported by the demonstration that Wortmannin, an inhibitor of PI 3-kinase, stimulates SAP kinase activity. The finding that Wortmannin treatment is also associated with internucleosomal DNA fragmentation may support a potential link between PI 3-kinase and regulation of both SAP kinase and programmed cell death.

L8 ANSWER 13 OF 38 CA COPYRIGHT 2002 ACS
AU Liao, Ching-Len; Lai, Michael M. C.
SO Virology (1995), 209(2), 428-36
CODEN: VIRLAX; ISSN: 0042-6822
PY 1995
AB Mouse hepatitis virus (MHV), a coronavirus, generates defective-interfering (DI) RNAs of different sizes during passages at high multiplicities of infection. All MHV DI RNAs characterized so far contain an open reading frame (ORF) encoding a fused viral protein; in addition, DI RNAs with a long ORF have a competitive advantage over those with a shorter ORF. These findings suggest that DI RNA replication may require an ORF encoding a **cis-acting** viral **protein**. A 12-nucleotide (nt) amber-mutation linker was inserted at various positions in a naturally occurring DI RNA to truncate the ORF. Most of the mutants replicated as well as the wild-type DI RNA, irresp. of the presence or absence and the length of the ORF in the RNA. Sequence anal. showed that all of the mutants retained the insertional mutations even after 2 viral passages in tissue culture, establishing that the mutant D1 RNAs replicated. Further, two 3-nucleotide substitutions of the first two AUG codons of the ORF were introduced, thus completely closing the ORF. This DI RNA replicated as well as the wild-type DI, but, after a single passage, the majority of the mutant RNAs was replaced by recombinant RNAs which contain a restored functional ORF. However, an addnl. insertion of a 12-nt amber-mutation linker downstream of the AUG substitutions prevented recombination, and the DI RNA still replicated. These data indicate that DI RNA replication does not require a DI-specific ORF encoding cis-acting viral proteins and that a 12-nucleotide insertion could prevent or delay the occurrence of RNA recombination, suggesting the importance of direct or indirect RNA alignment in homologous RNA recombination.

L8 ANSWER 14 OF 38 CA COPYRIGHT 2002 ACS
AU Wlostowski, Tadeusz
SO Acta Biochimica Polonica (1994), 41(4), 359-65
CODEN: ABPLAF; ISSN: 0001-527X
PY 1994
AB A review and discussion with 61 refs. on general characteristics of metallothionein, **cis**- and trans-**acting** elements, activator **protein** 1, and calcium and metallothionein synthesis.

L8 ANSWER 15 OF 38 CA COPYRIGHT 2002 ACS
AU Black, Alexander C.; Ruland, Cristina T.; Luo, Jie; Bakker, Andreas; Fraser, John K.; Rosenblatt, Joseph D.
SO Virology (1994), 200(1), 29-41
CODEN: VIRLAX; ISSN: 0042-6822
PY 1994
AB The shift from viral regulatory to structural gene expression in human T-cell leukemia virus types I (HTLV-I) and II (HTLV-II) is mediated by Rex. The authors have have previously shown that HTLV-II Rex acts through

an element in R/U5 of the 5'-long terminal repeat (LTR), the Rex-responsive element (R+RE), and that Rex protein binds to specific RNA sequences, the Rex binding element (RBE), contained within the R+RE (Black et al., J. Virol. 65, 6645-6653, 1991b). Rex action through the RBE (nt 405-520) overcomes the inhibition of expression conferred by a contiguous LTR RNA regulatory element, which contains cis-acting repressive sequences (CRS; nt 520-630) that are not bound by Rex protein (Black et al., Virol., 181, 433-444, 1991a). The authors now show by electrophoretic mobility shift assay (EMSA) that cellular proteins in a HeLa nuclear extract bind specifically to RNA transcripts containing the HTLV-II CRS. Using UV (uv) crosslinking of gel-retarded bands, the authors identified a major protein species of approx. 60 kDa, p60CRS, that binds to CRS RNA and, with weaker affinity, to RBE RNA. In addition, a distinct 40-kDa protein, p40CRS, binds to U5 RNA (nt 645-750) downstream from the CRS. Specific deletions within CRS RNA can reduce or abrogate binding to this 60-kDa protein. EMSA and uv crosslinking assays also suggest that both p60CRS and p40CRS interact with CRS RNA. CRS function in a 5' LTR-linked gene expression assay correlates with the ability of both p60CRS and p40CRS to interact with 5' LTR RNA in vitro.

L8 ANSWER 16 OF 38 CA COPYRIGHT 2002 ACS
AU Glass, Michael John
SO (1992) 160 pp. Avail.: Univ. Microfilms Int., Order No. DA9304464
From: Diss. Abstr. Int. B 1993, 53(9), 4502
PY 1992
AB Unavailable

L8 ANSWER 17 OF 38 CA COPYRIGHT 2002 ACS
AU Zapp, Dirk; Bartkowski, Sigrid; Holewa, Beatrix; Zoidl, Christiane; Klein-Hitpass, Ludger; Ryffel, Gerhart U.
SO Molecular and Cellular Biology (1993), 13(10), 6416-26
CODEN: MCEBD4; ISSN: 0270-7306
PY 1993
AB LFB1 (HNF1) is a tissue-specific transcription factor found in the livers, stomachs, intestines, and kidneys of vertebrates. By analyzing the promoter of the Xenopus LFB1 gene, the authors identified potential autoregulation by LFB1 and regulation by HNF4, a transcription factor with a tissue distribution similar to that of LFB1. Injection of LFB1 promoter-chloramphenicol acetyltransferase constructs into Xenopus eggs revealed embryonic activation that is restricted to the region of the developing larvae expressing endogenous LFB1. Proper embryonic activation was also observed with a rat LFB1 promoter. Deletion anal. of the Xenopus and rat promoters revealed that in both promoters embryonic activation is absolutely dependent on the presence of an element that contains CCNCTCTC as the core consensus sequence. Since this element is recognized by the maternal factor OZ-1 previously described by N. Ovsenek, et al., (1992), the authors might have identified the main constituents of a hierarchy that leads via LFB1 to the activation of tissue-specific genes during embryogenesis.

L8 ANSWER 18 OF 38 CA COPYRIGHT 2002 ACS
AU Wera, Stefaan; Belayew, Alexandra; Martial, Joseph A.
SO Molecular Endocrinology (1993), 7(8), 965-71

CODEN: MOENEN; ISSN: 0888-8809
PY 1993
AB Human PRL (hPRL) gene expression is controlled by cAMP and Ca2+. This control is mediated by two cis-elements: a Pit-1 binding site (-62 to -35) and sequence A (-110 to -85), present in the hPRL promoter. The authors have investigated whether protein phosphatases could be involved in this regulation. GC-type rat pituitary tumor cells were transfected with sequence -138 to -35 of the hPRL gene promoter, upstream from a thymidine kinase promoter and a chloramphenicol acetyltransferase (CAT) reporter gene. Addition of okadaic acid (OA), a specific inhibitor of protein phosphatases 1 and 2A, stimulates transient expression of the CAT gene. The dose-response curve shows a maximal effect at 25 nM OA (2.2-fold stimulation above controls). The OA effect is also observed with a natural 4500-base pair hPRL promoter. A single copy of the hPRL promoter sequence -115 to -85 (sequence A) confers to a thymidine kinase-CAT construct an identical response to OA, whereas a single copy of the proximal Pit-1 binding site does not. Synergism is observed between cAMP and OA in activating PRL gene transcription. This synergism is also observed with a single copy of sequence A. The effect of cAMP is not mediated by an L-type Ca2+ channel, since addition of the Ca2+ channel antagonist verapamil does not decrease it, nor does complexing extracellular Ca2+ significantly reduce it. Furthermore, OA and the Ca2+ channel opener BAY K8644 exert additive effects.

L8 ANSWER 19 OF 38 CA COPYRIGHT 2002 ACS
AU Ponnazhagan, S.; Kwon, Byoung G.
SO Pigment Cell Research (1992), 5(4), 155-61
CODEN: PCREEA; ISSN: 0893-5785
PY 1992
AB The tyrosinase gene is specifically expressed in melanocytes. Understanding the mol. basis of tissue-specific expression of the tyrosinase gene will greatly explain the mechanisms controlling pigmentation. The authors report a nucleotide sequence TGATGTATTC, located -236 base pairs upstream of the transcription start site, that enhances tyrosinase gene expression in mouse melanoma cells. The sequence is referred to as the tyrosinase element-1 (TE-1). TE-1 was protected from DNAase I cleavage by pigment cell nuclear exts. but was not protected by non-pigment cell nuclear extract Partial purification of TE-1 binding protein (TEBP-1) was performed from the B16 mouse melanoma cell nuclear extract using biotin-cellulose affinity chromatog. The affinity-purified fraction exhibited binding to the DNA fragment containing TE-1, and to a synthetic oligomer representing TE-1. UV-crosslinking indicated that the size of TEBP-1 is approx. 49 kD. TE-1 also directed enhanced CAT activity in the B16 melanoma cells but not in non-pigment cells. TE-1 may be an enhancer element that is responsible for pigment cell specific expression of the tyrosinase gene.

L8 ANSWER 20 OF 38 CA COPYRIGHT 2002 ACS
AU Chen, Shu Guang; Kulju, David; Halt, Sean; Murakami, Kentaro
SO Biochemical Journal (1992), 284(1), 221-6

CODEN: BIJOAK; ISSN: 0306-3275
PY 1992
AB A long-chain neutral phospholipid, dioleoylphosphatidylcholine, was found to support protein kinase C activation by cis-fatty acid and diacylglycerol (DAG). This effect of phosphatidylcholine (PC) is totally dependent on the presence of cis-fatty acid; PC greatly stimulates the cis-fatty acid-induced protein kinase C activity, but it does not activate protein kinase C at all, even in the presence of DAG, if cis-fatty acid is absent. DAG, however, plays a modulatory role in the presence of Ca2+; it further enhances the PC-potentiated **cis**-fatty acid **activation** of **protein** kinase C. Although the activities of all three protein kinase C subtypes tested (types I, II and III) are supported by this PC mechanism, type III is most sensitive to the DAG effect, and it is activated synergistically by cis-fatty acid and DAG. The potency of PC to support the synergistic activation of this subtype is equivalent to that of phosphatidylserine (PS). There are several differences, however, between PC- and PS-supported synergism observed in type III protein kinase C: (1) Ca2+-sensitivity is different; PC requires higher concns. of Ca2+ (10-20 μm-Ca2+) than those required for PS (micromolar Ca2+); (2) PC/cis-fatty acid/DAG-induced autophosphorylation of protein kinase C subtypes (types I, II and III) is very weak, whereas PS/cis-fatty acid/DAG strongly stimulate autophosphorylation of these subtypes under the conditions at which both PC and PS systems fully activate the protein kinase C in terms of histone phosphorylation. These observations suggest that a neutral phospholipid such as PC may also participate in the activation and differential regulation of protein kinase C.

L8 ANSWER 21 OF 38 CA COPYRIGHT 2002 ACS
AU Liddell, Susan; Bownes, Mary
SO Molecular and General Genetics (1991), 230(1-2), 219-24
CODEN: MGGEAE; ISSN: 0026-8925
PY 1991
AB The regulatory sequences leading to the ovarian and fat body expression of yolk proteins 1 and 2 (YP1 and 2) of D. melanogaster have been characterized in some detail. These genes (yp1 and yp2) share many enhancer elements, and some important regulatory sequences lie within the coding regions. This report describes an initial investigation of the cis-regulation of the gene encoding yolk protein 3 (yp3). A system is described for P element transformation using the complete and unaltered yp3 gene rather than reporter genes, and sequences are described which confer correct expression in the ovary and carcass.

L8 ANSWER 22 OF 38 CA COPYRIGHT 2002 ACS
AU Glasser, Stephan W.; Korfhagen, Thomas R.; Wert, Susan E.; Bruno, Michael D.; McWilliams, Karen M.; Vorbroker, Diane K.; Whitsett, Jeffrey A.
SO American Journal of Physiology (1991), 261(4, Pt. 1), L349-L356
CODEN: AJPHAP; ISSN: 0002-9513
PY 1991
AB Transgenic mice bearing chimeric genes consisting of 5'-sequences derived from the human surfactant protein C (SP-C) gene and the bacterial chloramphenicol acetyltransferase (CAT) gene were generated. Anal. of CAT

activity was utilized to demonstrate tissue-specific and developmental expression of chimeric genes. Lung-specific expression of the 3.7 SP-C-CAT transgene was observed in eight distinct transgenic mouse lines. Expression of the 3.7 SP-C-CAT transgene was first detected in fetal lung on day 11 of gestation and increased dramatically with advancing gestational age, reaching adult levels of activity before birth. In situ hybridization demonstrated that expression of 3.7 SP-C-CAT mRNA was confined to the distal respiratory epithelium. Antisense CAT hybridization was detected in bronchiolar and type II epithelial cells in the adult lung of the 3.7 SP-C-CAT transgenic mice. In situ hybridization of four distinct 3.7 SP-C-CAT transgenic mouse lines demonstrated bronchiolar-alveolar expression of the chimeric CAT gene, although the relative intensity of expression at each site varied within the lines studied. Glucocorticoids increased murine SP-C mRNA in fetal lung organ culture. Likewise, expression of 3.7 SP-C-CAT transgene increased during fetal lung organ or explant culture and was further enhanced by glucocorticoid in vitro. The 5'-regions of human SP-C conferred developmental, lung epithelial, and glucocorticoid-enhanced expression of bacterial CAT in transgenic mice. The increased expression of SP-C accompanying prenatal lung development and exposure to glucocorticoid is mediated, at least in part, at the transcriptional level, being influenced by cis-active elements contained within the 5'-flanking region of the human SP-C gene.

L8 ANSWER 23 OF 38 CA COPYRIGHT 2002 ACS
AU Lemaigre, Frederic P.; Durviaux, Serge M.; Rousseau, Guy G.
SO Molecular and Cellular Biology (1991), 11(2), 1099-106
CODEN: MCEBD4; ISSN: 0270-7306
PY 1991
AB The liver-type and muscle-type isoenzymes of 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase are encoded by a gene that uses 2 alternative promoters. **Cis-acting** sequences and **protein**-binding sites were identified on the liver-type promoter. Transfection assays with deleted promoters showed that maximal promoter activity is contained within 360 bp upstream of the cap site. DNase I footprinting expts. with liver and spleen nuclear exts. and with purified proteins revealed several protein-binding sites in this region. These included 4 binding sites for nuclear factor I, 1 site that contains an octamer consensus but showed a liver-specific footprint pattern, 2 liver-specific protein-binding sites, and 1 poly(dG)-containing binding site. Transfection of cells of hepatic origin suggested that all these sites except one are involved in transcriptional regulation. The region between -360 and -2663 contained an element that functioned as a silencer in a nonhepatic cell line. It is concluded that in liver transcription from the liver-type promoter of the 6-phosphofructo-2-kinase/fructose-3,6-bisphosphatase gene is controlled by ubiquitous and tissue-specific factors and involves activating and derepressing mechanisms.

L8 ANSWER 24 OF 38 CA COPYRIGHT 2002 ACS
AU Inouye, Sachiye; Gomada, Manabu; Sangodkar, U. M. X.; Nakazawa, Atsushi; Nakazawa, Teruko
SO Journal of Molecular Biology (1990), 216(2), 251-60
CODEN: JMOBAK; ISSN: 0022-2836
PY 1990
AB Transcription of the first operon coding for m-xylene-degrading enzymes on

the TOL plasmid of Pseudomonas putida is activated by the xylR gene product in the presence of m-xylene. The operon has the consensus sequence of the ntr/nif promoters at -24 and -12 regions, and the transcription is dependent on an RNA polymerase containing a sigma factor NtrA (RpoN or σ54). Deletion derivs. of the upstream sequence of the operon promoter were made in vitro and connected with the xylE gene on a plasmid. Their promoter activities were analyzed in Escherichia coli by monitoring catechol 2,3-dioxygenase activity, the xylE gene product. A cis-acting DNA element was identified which is required for activation of the operon promoter by XylR protein in the presence of the inducer. This regulatory sequence of about 40 base pairs in length was located 150 base pairs upstream from the transcription start site. Anal. of the mutants containing insertions between the upstream regulatory sequence and the promoter sequence demonstrated strong dependence of the activation upon helical periodicity of DNA. The regulatory sequence functioned in the inverse orientation or at a distance of more than 1 + 103 base pairs upstream from the promoter though less efficient. These results indicated that this upstream regulatory sequence might be the binding site for XylR protein. DNA loop formation through protein-protein interaction between XylR protein attached to the upstream sequence and the NtrA-containing RNA polymerase bound by the promoter sequence was suggested for activation of the operon transcription. A sequence similar to the regulatory sequence of the first operon of xylene metabolism was found in the upstream region of the xylS gene, which is also activated by XylR protein in the presence of m-xylene.

L8 ANSWER 25 OF 38 CA COPYRIGHT 2002 ACS
AU Karlsson, Olof; Thor, Stefan; Norberg, Torbjoern; Ohlsson, Helena; Edlund, Thomas
SO Nature (London, United Kingdom) (1990), 344(6269), 879-82
CODEN: NATUAS; ISSN: 0028-0836
PY 1990
AB The activity of the rat insulin I gene enhancer is mainly dependent on two **cis-acting protein**-binding domains. Here, the isolation of a cDNA encoding a protein, Isl-1, that binds to one of these domains is reported. Isl-1 contains a homeodomain with greatest similarity to those of the Caenorhabditis elegans proteins encoded by mec-3 and lin-11. In addition, Isl-1, like the lin-11 and mec-3 gene products, contains a novel Cys-His domain which is reminiscent of known metal-binding regions. Together these proteins define a novel class of proteins containing both a homeo- and a Cys-His-domain. Isl-1 is preferentially expressed in cells of pancreatic endocrine origin. If the structural homologies between Isl-1 and the C. elegans gene products reflect functional similarities, a role for Isl-1 in the development of pancreatic endocrine cells could be envisaged.

L8 ANSWER 26 OF 38 CA COPYRIGHT 2002 ACS
AU Weiss, Robert B.; Huang, Wai Mun; Dunn, Diane M.
SO Cell (Cambridge, MA, United States) (1990), 62(1), 117-26
CODEN: CELLB5; ISSN: 0092-8674
PY 1990
AB Phage T4 DNA topoisomerase gene 60 contains a 50 nucleotide untranslated region within the coding sequence of its mRNA. Translational bypass of this sequence by elongating ribosomes has been postulated for the mode of

synthesis of an 18 kd polypeptide specified by the split coding segments. Ribosome bypass of the untranslated region also occurs when a segment of gene 60 is fused to lacZ and expressed in Escherichia coli. The efficiency of bypass in these gene 60-lacZ fusions approaches 100%. Here, mutations that delete, insert, or substitute nucleotides from gene 60-lacZ fusions are examined Essential features necessary for high level gap bypass emerging from this anal. are a **cis-acting** nascent **peptide** sequence, a short duplication bordering the gap, and a stop codon contained in a stem-loop structure at the 5' junction of the gap.

L8 ANSWER 27 OF 38 CA COPYRIGHT 2002 ACS
AU Hagino-Yamagishi, Kimiko; Nomoto, Akio
SO Journal of Virology (1989), 63(12), 5386-92
CODEN: JOVIAM; ISSN: 0022-538X
PY 1989
AB To construct poliovirus defective interfering (DI) particles in vitro, an RNA was synthesized from a cloned poliovirus cDNA, pSM1(T7)1, which carried a deletion in the genome region corresponding to nucleotide positions 1663 to 2478 encoding viral capsid proteins, by using bacteriophage T7 RNA polymerase. The RNA was designed to retain the correct reading frame in nucleotide sequence downstream of the deletion. HeLa S3 monolayer cells were transfected with the deletion RNA and then superinfected with standard virus as a helper. The DI RNA was observed in the infected cells after three passages at high multiplicity of infection. The sequence anal. of RNA extracted from the purified DI particle clearly showed that this DI RNA had the same deletion in size and location as that in the RNA used for the transfection. Thus, the authors succeeded in construction of a poliovirus DI particle in vitro. To gain insight into the mechanism for DI generation, the authors constructed poliovirus cDNAs pSM1(T7)1a and pSM1(T7)1b that, in addition to the same deletion as that in pSM1(T7)1, had insertion sequences of 4 bases and 12 bases, resp., at the corresponding nucleotide position, 2978. The RNA transcribed from pSM1(T7)1a was not a template for synthesis of poliovirus nonstructural proteins and therefore was inactive as an RNA replicon. On the other hand, the RNA from pSM1(T7)1b replicated properly in the transfected cells. Superinfection of the transfected cells with standard virus resulted in production of DI particles derived from pSM1(T7)1b and not from pSM1(T7)1a. These observations indicate that deletion RNAs that are inactive replicons have little or no possibility of being genomes of DI particles, suggesting the existence of a nonstructural protein(s) that has an inclination to function as a **cis-acting protein**(s). The method described here will provide a useful technique to investigate genetic information essential for poliovirus replication.

L8 ANSWER 28 OF 38 CA COPYRIGHT 2002 ACS
AU LaMarco, Karen L.; McKnight, Steven L.
SO Genes & Development (1989), 3(9), 1372-83
CODEN: GEDEEP; ISSN: 0890-9369
PY 1989

AB Expression of herpes simplex virus type 1 (HSV1) immediate early (IE) genes is activated by a polypeptide component of the mature virion termed viral protein 16 (VP16). Stimulation of IE expression by VP16 operates via 2 cis-regulatory sequences: TAATGARAT (R = purine), and the purine-rich hexanucleotide sequence GCGGAA. VP16 does not bind directly to either of the IE cis-regulatory sequences. Rather, these elements appear to represent binding sites for host cells proteins. Herein, the purification of a host cell (liver) factor that binds to the GCGAA motif is reported. This factor (EIFga) is capable of binding in vitro to an oligomerized form of the hexanucleotide sequence GAAACG, which is common to a variety of virus- and interferon-inducible genes. The GAAACG repeats of interferon- and virus-inducible genes, and the GA-rich repeats of HSV1 IE genes confer similar functional properties when appended to the promoter of a heterologous gene. These observations raise the possibility that HSV1 may activate its IE genes in a manner that exploits one of the components used by mammalian cells to combat virus infection.

L8 ANSWER 29 OF 38 CA COPYRIGHT 2002 ACS
AU Linden, David J.; Routtenberg, Aryeh
SO Journal of Physiology (Cambridge, United Kingdom) (1989), 419, 95-119
CODEN: JPHYA7; ISSN: 0022-3751
PY 1989
AB To determine if cis-fatty acids, protein kinase C (PKC)-activating compds. would modulate ionic currents, the whole-cell voltage-clamp technique was applied to N1E-115 neuroblastoma cells. Anal. of families of currents evoked under voltage clamp by depolarizing steps from a holding potential of -85 mV during external application of 5 μM oleate (a cis-fatty acid) showed a 36% reduction of the peak inward current with no shift in either the peak or the reversal potential of the current-voltage relation and no alteration of outward current. External application of the cis-fatty acids oleate, linoleate, and linolenate reversibly attenuated voltage-dependent Na+ current with approx. half-maximal dose values of 2, 3, and 10 μM, resp. Oleate was .apprx.2-fold more potent when applied internally (ED53 = 1 μM). Externally applied elaidate (a trans-isomer of oleate) and stearate (a saturated fatty acid), which do not activate PKC, had no effect. Since cis-fatty acids are known to fluidize membranes, as well as to activate PKC, these functions were dissociated by applying compds. that fluidize membranes but do not activate PKC: methyloleate and lysophosphatidylcholine. Neither compound affected Na+ current when applied externally at concns. of 1-50 μM. In contrast to cis-fatty acids, three classical PKC activators, phorbol-12,13-dibutyrate (PDB), phorbol-12,13-diacetate (PDA), and 1,2-oleoylacetylglycerol (OAG) had no effect on the voltage-dependent Na+ current when applied externally at 10 nM-1 μM (phorbol esters) or 1-150 μM (OAG) for incubation periods ≤1 h. External application of the PKC inhibitors polymyxin B, H-7, sphingosine, and staurosporine blocked the attenuation of the Na+ current by cis-fatty acids in a dose-dependent manner, with maximal inhibition occurring at doses of 50, 10, 200, and 0.1 μM, resp. The cyclic nucleotide-dependent protein kinase inhibitor H-8 was much less effective in blocking the cis-fatty acid effect. Polymyxin B and staurosporine were more potent when applied internally. Chronic (24 h) exposure to 1 μM

TPA was employed to down-regulate PKC. This treatment did not alter the baseline characteristics of the isolated Na+ current, but was effective in blocking the attenuation of Na+ current produced by subsequent external application of cis-fatty acids. To determine whether the distinction between cis-fatty acids and classical PKC activators was specific to the Na+ current, these compds. were applied externally to isolated Ca2+ currents. Both classes of compound attenuated both transient and sustained Ca2+ currents without altering their kinetics of activation. cis-Fatty acids, but not the classical activators, were significantly more potent with internal application. Inhibitors of PKC blocked the effect of externally applied cis-fatty acids and were more potent with internal application. These data suggest 2 broad classes of explanation. First, cis-fatty acid attenuation of the Na+ current could be mediated in part through a non-PKC mechanism. The 2nd explanation, which is favored by the authors, is that activation of the PKC family of enzymes by cis-fatty acids and the classical PKC activators could result in different patterns of substrate phosphorylation, such that cis-fatty acid activation of PKC produces attenuation of the Na+ current in N1E-115 cells, whereas stimulation of PKC by classical activators does not.

L8 ANSWER 30 OF 38 CA COPYRIGHT 2002 ACS
AU Dong, Xinnian; Womble, David D.; Rownd, Robert H.
SO J. Mol. Biol. (1988), 202(3), 495-509
CODEN: JMOBAK; ISSN: 0022-2836
PY 1988
AB Segment-directed mutagenesis was used to isolate a temperature-sensitive mutant of the gene that encodes the **cis-acting** RepA1 initiation **protein** of the IncFII plasmid NR1. The mutant protein was unable to promote initiation of plasmid replication in vivo at 42°. Both the wild-type and the mutant repA1 genes were cloned sep. into the high-expression vector plasmid pAS1. In these pAS1-repA1 derivs., the transcription of the repA1 gene was under the control of the λPL promoter, which was regulated by the temperature-sensitive λcI857 repressor protein. The translation initiation of the repA1 mRNA from these derivs. was mediated by the λcII Shine-Dalgarno sequence and initiation codon. The yield of 33,000 Mr RepA1 protein detected on SDS/polyacrylamide gels from Escherichia coli cells containing the pAS1-repA1 derivs. was dependent upon whether the newly synthesized RepA1 was capable of interacting in cis with the downstream NR1 replication origin on the cloned DNA fragment. Mutations in the RepA1 gene or deletions of the cis origin region dramatically increased the detectable yield of RepA1 protein. Deletion of the NR1 origin region from the pAS1 derivative containing the wild-type repA1 gene enabled the **cis-acting** RepA1 **protein** to complement partially the temperature-sensitive repA1 mutant in trans, to increase the copy number in trans of plasmids that contained the NR1 replicon, and to help NR1 derivs. overcome plasmid incompatibility. The trans effects of RepA1 provided by the pAS1-repA1 derivs. that retained the origin in cis were much less significant. RepA1 provided in trans also stimulated the replication of plasmids carrying cloned copies of the NR1 replication origin region regardless of whether the origin was transcribed from an upstream promoter.

L8 ANSWER 31 OF 38 CA COPYRIGHT 2002 ACS
AU Masai, Hisao; Arai, Kenichi
SO Nucleic Acids Res. (1988), 16(14A), 6493-514
CODEN: NARHAD; ISSN: 0305-1048
PY 1988
AB Initiation of R1 plasmid replication is dependent on **cis-acting** repA **protein** and the 188 base-pair (bp) sequence, oriR. The repA protein synthesized in vitro preferentially activates oriR in cis, regardless of the orientation and location of oriR on the template DNA. The repA protein is not reusable after it activates oriR in the cis-position. The **cis-action** of repA **protein** is also dependent on the presence of CIS, a 170-bp sequence, between repA and oriR. CIS Contains a rho-dependent transcription terminator of the repA transcript, deletion of which results in decrease in transformation efficiency and rapid loss of plasmid in the absence of selection. The significance of transcription termination events in replication was indicated by decreased replication activity in vivo caused by premature termination of the repA transcript between repA and CIS. A model which may account for the role of CIS in mediating the cis-action of the repA protein is presented.

L8 ANSWER 32 OF 38 CA COPYRIGHT 2002 ACS
AU Womble, David D.; Rownd, Robert H.
SO J. Mol. Biol. (1986), 192(3), 529-48
CODEN: JMOBAK; ISSN: 0022-2836
PY 1986
AB A quant. model for the regulation of replication of the low copy number IncFII plasmid NR1 in the Escherichia coli cell division cycle has been developed. The initiation of NR1 replication requires a **cis-acting** initiator **protein** whose synthesis is regulated by several mechanisms. The NR1 regulatory processes include co-operative protein-protein interactions in the formation of an active transcription repressor, the interaction of repressor with a rightward operator site in the control of transcription of the initiator gene, and the interaction of an inhibitor RNA transcript with the initiator mRNA in the control of translation of the initiation protein. A statistical thermodn. model was used to predict probable configurations of the regulatory processes in a single growing cell. These probabilities were coupled by a kinetic model to the events of the cell cycle, such as initiation of mRNA transcription and protein translation, and the initiation of plasmid DNA replication. Parameter values were chosen so that the simulated values for plasmid copy number and the intracellular concns. of repressor protein and mRNA agreed with exptl. determined ests. A number of different copy number mutants that have altered one or another of the regulatory processes were simulated by the model. The contributions of each of the regulatory processes toward the overall stability of inheritance of plasmid NR1 in a population of cells in culture were examined These simulations predict a very stable pattern of inheritance for plasmid NR1 despite its low copy number, in agreement with exptl. observation.

L8 ANSWER 33 OF 38 CA COPYRIGHT 2002 ACS
AU Raleigh, Elisabeth A.; Kleckner, Nancy
SO J. Mol. Biol. (1984), 173(4), 437-61

CODEN: JMOBAK; ISSN: 0022-2836
PY 1984
AB The occurrence of multiple transposon-promoted chromosomal rearrangements in E. coli K12 strains containing transposon Tn10 was studied. A single Tn10 element, with its 2 closely spaced insertion sequence (IS10) elements, frequently gives rise to complex rearrangements that can be accounted for as the sum of 2 classical IS10 events. Using a strain containing differentially marked Tn10 elements at widely separated locations, the possibility was investigated that IS10-promoted rearrangements occur in cell-wide bursts, as expected if cells could occasionally undergo brief periods when all IS10 transposition events were activated, interspersed with longer periods of relative quiescence. No evidence for strong (>60-fold), periodic cell-wide activation was found. Several mechanisms were discussed by which 2 closely linked IS10 elements could undergo coupled double events without cell-wide activation: local activation of small chromosomal regions, periodic bursts of synthesis of **cis-acting** transposase **protein**, and(or) a propensity for elements that have actually engaged in one rearrangement event to initiate a 2nd successive event immediately thereafter.

L8 ANSWER 34 OF 38 CA COPYRIGHT 2002 ACS
AU Tyler, Brett M.; Geever, Robert F.; Case, Mary E.; Giles, Norman H.
SO Cell (Cambridge, Mass.) (1984), 36(2), 493-502
CODEN: CELLB5; ISSN: 0092-8674
PY 1984
AB The function of the qa-1F pos. regulatory gene of Neurospora was studied by mapping the initiation sites for transcription of the clustered qa structural genes in wild type, in qa-1F mutants, and in **cis-acting activator protein**-independent mutants of qa-2(qa-2ai mutants). Each structural gene under qa-1F control has 2-4 promoters. The qa-2ai mutations, which include point mutations and small (68-84-base-pair) duplications 5' to qa-2, allow qa-1F-independent transcription from surrounding qa promoters independently of the orientations and positions (upstream or downstream) of the mutations relative to the promoters. However, 1 subset of promoters was not reactivated by the enhancer-like elements created by these mutations, and qa-1F mutants selectively deficient in the activation of these promoters were identified. Therefore, the qa-1F regulatory gene appears to control 2 types of promoters that have different requirements for activation.

L8 ANSWER 35 OF 38 CA COPYRIGHT 2002 ACS
AU Grindley, Nigel D. F.; Joyce, C. M.
SO Cold Spring Harbor Symp. Quant. Biol. (1981), 45(1, Movable Genet. Elem.), 125-33
CODEN: CSHSAZ; ISSN: 0091-7451
PY 1981
AB A 1050-base-pair inverted repeat of Tn903 acted as an insertion sequence element (designated IS903). A Tn903 derivative was constructed which lacks a 520-base-pair segment in 1 of its 1050-base-pair inverted repeats; the derivative could still transpose. Insertion mutation data correlation with the DNA sequence of the inverted repeat suggested that translation of a 921-base-pair coding frame, entirely within the 1050-base-pair repeat, is required for transposition. Anal. of replicon fusions mediated by the partially deleted derivative Tn903δ1 suggested that the Tn903

transposase is a **cis-acting protein**. A partial DNA sequence for Tn903 is presented.

L8 ANSWER 36 OF 38 CA COPYRIGHT 2002 ACS
AU Ikeda, Johe; Yudelevich, Arturo; Shimamoto, Nobuo; Hurwitz, Jerard
SO J. Biol. Chem. (1979), 254(19), 9416-28
CODEN: JBCHA3; ISSN: 0021-9258
PY 1979
AB Gene A of the .vphi.X174 genome codes for 2 proteins, A and A*. These 2 proteins were purified to homogeneity as judged by Na dodecyl sulfate-polyacrylamide gel electrophoresis. In addition to the known endonuclease activity, the .vphi.X A protein also caused relaxation of supertwisted .vphi.XRFI DNA and formation of a .vphi.XRFII DNA·.vphi.X A protein complex which has a discontinuity in the A cistron of the viral strand. This isolatable complex supported DNA synthesis when supplemented with exts. of uninfected Escherichia coli which lack .vphi.X A protein and .vphi.XRFI DNA. The .vphi.XRFII DNA·.vphi.X A protein complex was attacked by exonuclease III but was not susceptible to attack by E. coli DNA polymerase I, indicating that the 5'-end of the complex is blocked. The .vphi.X A protein did not act catalytically in the cleavage of .vphi.XRFI DNA. Under conditions leading to the quant. cleavage of .vphi.XRFI DNA, the molar ratio of .vphi.XRFI DNA to added .vphi.X A protein was .apprx.1:10. At this molar ratio, crosslinking expts. with di-Me suberimidate yielded 10 distinct protein bands which were multiples of the monomeric ϕX A protein. In the absence of DNA or in the presence of inactive DNA (.vphi.XRFII DNA), no distinct protein bands above a trimer were detected. It was possible in vitro to form a .vphi.XRFII DNA·.vphi.X A protein complex with wild-type .vphi.XRFI DNA (.vphi.X A gene+) and with .vphi.XRFI DNA isolated from E. coli (su+) infected with phage .vphi.X H90 (an am mutant in the .vphi.X A gene). Thus, in vitro, in contrast to in vivo studies, .vphi.X A protein is not a **cis acting protein**. The purified .vphi.X A* protein did not substitute for the .vphi.X A protein in in vitro replication of .vphi.XRFI DNA nor did it interfere with the action of the .vphi.X A protein which binds only to supertwisted .vphi.XRFI DNA. In contrast, the .vphi. A* protein bound to all duplex DNA prepns. tested. This property prevents nucleases of E. coli from hydrolyzing duplex DNAs to small mol. weight products.

L8 ANSWER 37 OF 38 CA COPYRIGHT 2002 ACS
AU Abrescia, Paolo; Guardiola, John; Foresti, Magda; Lamberti, Alessandro; Iaccarino, Maurizio
SO Mol. Gen. Genet. (1979), 171(3), 261-75
CODEN: MGGEAE; ISSN: 0026-8925
PY 1979
AB The effect of mutations in 3 genes, ilvO, ilvA, and rho, on the expression of the ilvEJGDA gene cluster of E. coli K-12 is analyzed. The ilvO603 mutation causes a cis-dominant derepression of the ilvEJGD genes. In particular, the ilvG gene, not expressed in the wild type, becomes expressed in the ilvO603 strain. Introduction of ilvA mutations (ilvA454 or ilvA628) in the ilvO603 strain showed that ilvG expression requires the presence in cis of both an ilvO603 mutation and of an ilvA+ allele. The ilvG gene is not expresses when an ilvO+, ilvA+ genotype is present in trans. However, it is expressed when the chromosome in trans is ilvO603, ilvA+ (ilvG-). Apparently, ilvO603 is part of ilvA, the structural gene for threonine deaminase, and threonine deaminase from the ilvO603 mutant

binds the ilvO603 site and not the ilvO+ site. Thus, the ilvA gene product would be a **cis-acting protein**. Mutations in the rho gene cause derepression of the ilvEJGDA gene cluster without a concomitant expression of the ilvG gene. Introduction of either a rHO-218 or a rho-115 mutation into the ilvO603, ilvA454 double mutant causes expression of ilvG. Thus, the ilvA gene product, threonine deaminase, is involved in termination of transcription as an antagonist of the rho gene product. Introduction of ilvA454 into an ilvO603 strain causes also a decrease in expression of the ilvE, ilvJ, and ilvD genes. This effect is maximum in the case of the ilvD gene and was studied in detail in isogenic strains containing also the rho-218 mutation. A regulatory model which correlates these results is presented.

L8 ANSWER 38 OF 38 CA COPYRIGHT 2002 ACS
AU Lindahl, Gunnar; Hirota, Yukinori; Jacob, Francois
SO Proc. Nat. Acad. Sci. U. S. (1971), 68(10), 2407-11
CODEN: PNASA6
PY 1971
AB The temperaturesensitive mutant CRT46 of E. coli K12 is unable to initiate new rounds of DNA replication at 42°. Mutants of bacteriophage P2 have been isolated, which, in the prophage state, allow mutant CRT46 to grow at 42°. The lysogenic bacteria that grow at 42° are apparently replicating under the control of prophage P2, which substitutes for the bacterial initiation system. The ability of prophage P2 to cause this suppression phenomenon depends on the position of the prophage on the bacterial chromosome. Those lysogenic strains that are able to grow at 42°C all carry the prophage close to metE. The P2 mutants that allow CRT46 to grow at 42° have insertions in the early region of the P2 genome. The suppression requires the **cis-acting protein** formed by gene A of P2.

```
=> s in vitro
L9      501199 IN VITRO
                (VITRO)

=> s l9 and librar?
         61009 LIBRAR?
L10       4108 L9 AND LIBRAR?

=> s l10 and DNA(2w)bind?(4w)(peptide or polypeptide or protein)
        560869 DNA
        919423 BIND?
        273170 PEPTIDE
         86631 POLYPEPTIDE
       1411336 PROTEIN
          9004 DNA(2W)BIND?(4W)(PEPTIDE OR POLYPEPTIDE OR PROTEIN)
L11         61 L10 AND DNA(2W)BIND?(4W)(PEPTIDE OR POLYPEPTIDE OR PROTEIN)

=> s l11 not 1999-2002/py
      2767092 1999-2002/PY
L12         44 L11 NOT 1999-2002/PY
```

=> d l12 1-44 ti au so py ab

L12 ANSWER 1 OF 44 CA COPYRIGHT 2002 ACS
TI The ets family member Tel binds to the Fli-1 oncoprotein and inhibits its transcriptional activity
AU Kwiatkowski, Boguslaw A.; Bastian, L. Scot; Bauer, Thomas R., Jr.; Tsai, Schickwann; Zielinska-Kwiatkowska, Anna G.; Hickstein, Dennis D.
SO Journal of Biological Chemistry (1998), 273(28), 17525-17530
CODEN: JBCHA3; ISSN: 0021-9258
PY 1998
AB The tel gene, recently shown to be translocated in a spectrum of acute and chronic human leukemias, belongs to the ets family of sequence-specific transcription factors. To determine the role of Tel in normal hematopoietic development, we used the tel gene as the bait in the yeast two-hybrid system to screen a hematopoietic stem cell **library**. Two partners were identified: Tel binds to itself, and Tel binds to the ets family member Fli-1. In **vitro** and in vivo assays confirmed these interactions. In transient transfection assays, Fli-1 transactivates megakaryocytic specific promoters, and Tel inhibits this effect of Fli-1. Transactivation studies using deletion mutants of Tel, and the Tel-AML-1 fusion protein, indicate that the helix-loop-helix domain of Tel only partially inhibits transactivation and that complete inhibition requires the full-length Tel mol., including the DNA binding domain. The Tel and Fli-1 proteins are expressed early in hematopoiesis, and the inability of Tel fusion proteins such as Tel-AML-1 to counteract Fli-1 mediated transactivation may contribute to the malignant phenotype in human leukemias where this fusion protein is present.

L12 ANSWER 2 OF 44 CA COPYRIGHT 2002 ACS
TI Cloning and characterization of a novel sequence-specific single-stranded-**DNA-binding protein**
AU Bayarshaihan, Dashzeveg; Soto, Ricardo J.; Lukens, Lewis N.
SO Biochemical Journal (1998), 331(2), 447-452
CODEN: BIJOAK; ISSN: 0264-6021
PY 1998
AB The promoter region of the chicken α2(I) collagen gene contains a pyrimidine-rich element that is well conserved in different mammalian species. This sequence can also form an unusual DNA structure as shown by its sensitivity to SI nuclease in **vitro** and it lies in a region that is DNase I-hypersensitive only when this promoter is active. The authors have recently reported that fibroblast nuclear proteins, including chicken Y-box-binding protein 1, bind to this single-stranded pyrimidine-rich sequence. Here the authors report the isolation, from a chick embryo fibroblast cDNA expression **library**, of a partial cDNA clone encoding a previously unknown protein, designated SSDP (sequence-specific single-stranded **DNA-binding protein**), that binds this single-stranded sequence. This clone contains 1199 bp of chicken sequence and has a single long open reading frame that encodes 284 amino acid residues. The affinity-purified recombinant protein encoded by this cDNA binds sequence-specifically to the single-stranded pyrimidine sequence. This cDNA sequence lacks significant similarity to any known gene in the data banks, but it is highly conserved in expressed sequence tags derived from both mouse and human. The corresponding amino acid sequence is remarkably conserved, having 97% identity with mouse and human expressed sequences. The

corresponding mRNA is approx. 1800 nt in length and is expressed in both fibroblasts and chondrocytes. The high affinity of this protein for this conserved pyrimidine-rich region suggests that it might be involved in the transcriptional regulation of the α2(I) collagen gene.

L12 ANSWER 3 OF 44 CA COPYRIGHT 2002 ACS
TI cDNA cloning, recombinant expression and characterization of polypeptides with exceptional DNA affinity
AU Nehls, Peter; Keck, Thomas; Greferath, Ruth; Spiess, Eberhard; Glaser, Tova; Rothbarth, Karsten; Stammer, Hermann; Werner, Dieter
SO Nucleic Acids Research (1998), 26(5), 1160-1166
CODEN: NARHAD; ISSN: 0305-1048
PY 1998
AB Polypeptides remaining tightly associated with isolated genomic DNA are of interest with respect to their potential involvement in the topol. organization, and/or function of genomic DNA. Such residual DNA-polypeptide complexes were used for raising monoclonal antibodies by in **vitro** immunization. Screening of a murine λgt11 cDNA **library** with these antibodies released a pos. cDNA (MC1D) encoding a 16 kDa polypeptide. The cloned homologous human cDNA (HC1D) was identified in the dbest data base by partial sequence comparison, and it was sequenced full length. The cDNA-derived amino acid sequences comprise nuclear location signals but none of the known DNA-binding motifs. However, the recombinantly expressed proteins show in **vitro** DNA binding affinities. A polyclonal antiserum to the recombinant MC1D protein immunostains sub-nuclear structures, and it detects a residual 16 kDa polypeptide on western blots of DNA digests. These results support the conclusion that the cloned cDNAs reflect mRNAs encoding one of the chem.-resistant polypeptides which can be detected in isolated genomic DNA by sensitive techniques, e.g. by 125iodine labeling and SDS-PAGE.

L12 ANSWER 4 OF 44 CA COPYRIGHT 2002 ACS
TI IB1, a JIP-1-related nuclear protein present in insulin-secreting cells
AU Bonny, Christophe; Nicod, Pascal; Waeber, Gerard
SO Journal of Biological Chemistry (1998), 273(4), 1843-1846
CODEN: JBCHA3; ISSN: 0021-9258
PY 1998
AB JIP-1 is a cytoplasmic inhibitor of the c-Jun amino-terminal kinase activated pathway recently cloned from a mouse brain cDNA **library**. The authors report herein the expression cloning of a rat cDNA encoding a JIP-1-related nuclear protein from a pancreatic β-cell cDNA **library** that the authors named IB1 for Islet-Brain 1. IB1 was isolated by its ability to bind to GTII, a cis-regulatory element of the GLUT2 promoter. The IB1 cDNA encodes a 714-amino acid protein, which differs from JIP-1 by the insertion of 47 amino acids in the carboxyl-terminal part of the protein. The remaining 667 amino acids are 97% identical to JIP-1. The 47-amino acid insertion contains a truncated phosphotyrosine interaction domain and a putative helix-loop-helix motif. Recombinant IB1 (amino acids 1-714 and 280-714) was shown to bind in **vitro** to GTII. Functionally IB1 transactivated the GLUT2 gene. IB1 was localized within the cytoplasm and the nucleus of insulin-secreting cells or COS-7 cells transfected with an expression vector encoding IB1. Using a heterologous GAL4 system, the authors localized an activation domain of IB1 within the first 280 amino acids of the protein. These data demonstrate that IB1 is a **DNA**-

binding protein related to JIP-1, which is highly expressed in pancreatic β-cells where it functions as a transactivator of the GLUT2 gene.

L12 ANSWER 5 OF 44 CA COPYRIGHT 2002 ACS
TI A **DNA**-topoisomerase-II-**binding protein** with eight repeating regions similar to DNA-repair enzymes and to a cell-cycle regulator
AU Yamane, Kazuhiko; Kawabata, Masahiro; Tsuruo, Takashi
SO European Journal of Biochemistry (1997), 250(3), 794-799
CODEN: EJBCAI; ISSN: 0014-2956
PY 1997
AB A two-hybrid system was used to isolate factors that interact with the C-terminal region of DNA topoisomerase IIβ. A pos. clone isolated from a HeLa cDNA **library** encoded 1522 amino acid residues (mol. mass 170670). The protein, designated topoisomerase-IIβ-binding protein 1 (TopBP1), interacted with the C-terminal region of topoisomerase IIβ synthesized in **vitro**. A database search indicated that TopBP1 possessed eight regions similar to regions of Rad4, Cut5, Ect2, Rev1 and x-ray repair cross-complementing 1 (XRCC1) proteins and a region similar to auto-modification sites of poly(ADP-ribose) polymerase, suggesting that TopBP1 supported catalytic reactions of topoisomerase II through transient breakages of DNA strands.

L12 ANSWER 6 OF 44 CA COPYRIGHT 2002 ACS
TI Isolation and analysis of two cDNA clones from human lymphocyte expression **library** which induce DNA binding activity in **vitro**
AU Boiko, V. P.; Svetlova, M. P.; Sazeeva, N. R.; Shestopalov, B. N.; Ariga, H.; Iguchi-Ariga, S. M. M.; Tomilin, N. V.
SO Molekulyarnaya Genetika, Mikrobiologiya i Virusologiya (1997), (4), 29-31
CODEN: MGMVDU; ISSN: 0208-0613
PY 1997
AB Two cDNA clones are sequenced which were isolated from human lymphocyte expression **library** using Southwestern (DNA-binding) screening with 32P-labeled Alu DNA in the presence of 100-fold excess of unbalanced poly (dI-dC). In one of the sequenced clones (vb22) an open reading frame (ORF) is detected, encoding protein with a new potential DNA-binding (zinc finger) domain, and **DNA-binding** activity of the **protein** is directly confirmed after its expression (as GST-fusion protein) in Escherichia coli. The other sequenced clone (wa12) is partially homologous to 15EST sequences present in GenBank (Apr., 1996) and cloned from very different human tissues. Connection of these 15 overlapping GenBank sequences resulted in a longer sequence covering wa12 and having ORF potentially encoding a new 10 kDa polypeptide without any apparent DNA-binding domains. This connected sequence as well as wa12 sequence having only 65 amino acids ORF are unrecognizable by computer software as the protein-coding regions, and we suppose that wa12 transcripts possess DNA-binding activity. Homopyrimidine blocks in RNA longer than 12 nucleotides are known to bind mirror duplex DNA sequences to form triplexes whose stability is comparable to that of protein-DNA complexes, and human promoters contain many such blocks.

L12 ANSWER 7 OF 44 CA COPYRIGHT 2002 ACS
TI Protein-protein interactions among the Aux/IAA proteins
AU Kim, Jungmook; Harter, Klaus; Theologis, Athanasios
SO Proceedings of the National Academy of Sciences of the United States of

America (1997), 94(22), 11786-11791
CODEN: PNASA6; ISSN: 0027-8424
PY 1997
AB The plant hormone indoleacetic acid (IAA) transcriptionally activates early genes in plants. The Aux/IAA family of early genes encodes proteins that are short-lived and nuclear-localized. They also contain a putative prokaryotic βαα **DNA binding** motif whose formation requires **protein** dimerization. Here, we show that the pea PS-IAA4 and Arabidopsis IAA1 and IAA2 proteins perform homo- and heterotypic interactions in yeast using the two-hybrid system. Gel-filtration chromatog. and chem. crosslinking expts. demonstrate that the PS-IAA4 and IAA1 proteins interact to form homodimers in **vitro**. Deletion anal. of PS-IAA4 indicates that the βαα containing acidic C terminus of the protein is necessary for homotypic interactions in the yeast two-hybrid system. Screening an Arabidopsis λ-ACT cDNA **library** using IAA1 as a bait reveals heterotypic interactions of IAA1 with known and newly discovered members of the Arabidopsis Aux/IAA gene family. The new member IAA24 has similarity to ARF1, a transcription factor that binds to an auxin response element. Combinatorial interactions among the various members of the Aux/IAA gene family may regulate a variety of late genes as well as serve as autoregulators of early auxin-regulated gene expression. These interactions provide a mol. basis for the developmental and tissue-specific manner of auxin action.

L12 ANSWER 8 OF 44 CA COPYRIGHT 2002 ACS
TI The distribution of binding sites for centromere protein B (CENP-B) is partly conserved among diverged higher order repeating units of human chromosome 6-specific alphoid DNA
AU Sugimoto, Kenji; Furukawa, Kenji; Kusumi, Kayo; Himeno, Michio
SO Chromosome Research (1997), 5(6), 395-405
CODEN: CRRSEE; ISSN: 0967-3849
PY 1997
AB We previously reported the isolation of alphoid satellite clones from a human genomic **library** using a DNA immunopptn. with centromere protein B (CENP-B). Here, we have characterized the distribution of CENP-B-binding sites on the 3-kb BamH1 repeats of the cos2 clone. Using in situ hybridization, this alphoid satellite was located primarily at the centromeric region of chromosome 6. The functional binding sites were mapped by precipitating the restriction fragments with recombinant CENP-B in **vitro**. One repeat (2B3-11) consisted of 19 copies of alphoid monomer, eight of which possessed the binding sites, while another (2B3-9) consisted of 18 copies of the monomer, seven of which possessed the binding sites. The distribution of the sites was well conserved between them, except for the terminus. A similar anal. with the remaining 6-kb region suggested the presence of a continuous 1-kb region with regular spacing of EcoR1 sites and the CENP-B-binding sites. When the nucleotide sequence of 2B3-11 was compared with that of another chromosome 6-specific alphoid repeat (p308) that had been described previously, this 1-kb region was highly conserved between them. The distribution of the CENP-B binding sites and the order of alphoid monomers might define the folding of alphoid repeats in the centromeric region.

L12 ANSWER 9 OF 44 CA COPYRIGHT 2002 ACS
TI Characterization of a gene encoding a **DNA-binding protein** that interacts in **vitro** with vascular specific cis elements of the phenylalanine ammonia-lyase promoter
AU Seguin, Armand; Laible, Gotz; Leyva, Antonio; Dixon, Richard A.; Lamb, Christopher J.
SO Plant Molecular Biology (1997), 35(3), 281-291
CODEN: PMBIDB; ISSN: 0167-4412
PY 1997
AB A study of the expression of a bean phenylalanine ammonia-lyase (PAL) promoter/β-glucuronidase gene fusion in transgenic tobacco has shown that the PAL2 promoter has a modular organization. Expression of the PAL2 promoter in the vascular system involves pos. and neg. regulatory cis elements. Among these elements is an AC-rich motif implicated in xylem expression and a suppressing cis element for phloem expression. Using radiolabeled complementary oligonucleotides bearing the AC-rich motif, a cDNA clone encoding a **DNA-binding protein** has been isolated from a tobacco λgt11 expression **library**. This factor, named AC-rich binding factor (ACBF), showed binding specificity to the AC-rich region. The specificity of ACBF for the AC-rich region was also shown using a gel retardation assay with an ACBF recombinant protein extract The deduced amino acid sequence from ACBF contains a long repeat of glutamine residues as found in well characterized transcription factors. Interestingly, ACBF shared sequence similarity to conserved amino acid motifs found in RNA-binding proteins. Genomic gel blot anal. indicated the presence of a small gene family of sequences related to ACBF within the tobacco nuclear genome. Anal. of tobacco mRNA using the ACBF cDNA as probe showed that while ACBF mRNA was present in all tissues examined, the highest transcript accumulation occurred in stem tissues. The functional characteristics of the AC-rich sequence were examined in transgenic tobacco. A heptamer of the AC-rich sequence, in front of a minimal 35S promoter from cauliflower mosaic virus (-46 to +4), conferred specific expression in xylem.

L12 ANSWER 10 OF 44 CA COPYRIGHT 2002 ACS
TI The yeast nucleolar protein Cbf5p is involved in rRNA biosynthesis and interacts genetically with the RNA polymerase I transcription factor RRN3
AU Cadwell, Craig; Yoon, Hye-Joo; Zebarjadian, Yeganeh; Carbon, John
SO Molecular and Cellular Biology (1997), 17(10), 6175-6183
CODEN: MCEBD4; ISSN: 0270-7306
PY 1997
AB Yeast Cbf5p was originally isolated as a low-affinity centromeric **DNA binding protein**. Cbf5p also binds microtubules in **vitro** and interacts genetically with two known centromere-related protein genes (NDC10/CBF2 and MCK1). However, Cbf5p was found to be nucleolar and is highly homologous to the rat nucleolar protein NAP57, which coimmunoppts. with Nopp140 and which is postulated to be involved in nucleolar-cytoplasmic shuttling. The temperature-sensitive cbf5-1 mutant demonstrates a pronounced defect in rRNA biosynthesis at restrictive temps., while tRNA transcription and pre-rRNA and pre-tRNA cleavage processing appear normal. The cbf5-1 mutant cells are deficient in cytoplasmic ribosomal subunits at both permissive and restrictive temps. A high-copy-number yeast genomic **library** was screened for genes that suppress the cbf5-1 temperature-sensitive growth phenotype. SYC1

(suppressor of yeast cbf5-1) was identified as a multicopy suppressor of cbf5-1 and subsequently was found to be identical to RRN3, an RNA polymerase I transcription factor. A cbf5δ null mutant is not rescued by plasmid pNOY103 containing a yeast 35S rRNA gene under the control of a Pol II promoter, indicating that Cbf5p has one or more essential functions in addition to its role in rRNA transcription.

L12 ANSWER 11 OF 44 CA COPYRIGHT 2002 ACS
TI The avian C/EBPγ gene encodes a highly conserved leucine zipper transcription factor
AU Baglia, Laurel A.; Bowers, William J.; Ruddell, Alanna
SO Gene (1997), 190(2), 297-302
CODEN: GENED6; ISSN: 0378-1119
PY 1997
AB The C/EBP family of transcription factors regulates viral and cellular CCAAT/enhancer element-mediated transcription. We report the isolation and characterization of genomic and cDNA clones encoding avian CCAAT/enhancer-binding protein-γ (C/EBPγ). A partial cDNA clone for a C/EBP-related gene was previously identified by expression **library** screening for proteins binding the A1 CCAAT/enhancer motif from the avian leukosis virus long terminal repeat [W. Bowers and A. Ruddell (1992) J. Virol. 66, 6578-6586]. Addnl. cDNA and genomic clones were generated and sequenced to identify the complete protein coding sequence of this gene. Sequence anal. indicates that this gene encodes the avian homolog of C/EBPγ. As with the murine C/EBPγ homolog, the avian C/EBPγ gene is comprised of two exons, with the open reading frame encoded in exon 2. The 150-aa C/EBPγ protein is highly conserved, as the avian protein shows more than 80 identity with the murine and human homologs. The sequence of the initiation methionine (-3 caaAUGa +4) from the 150-aa open reading frame has a non-optimal Kozak initiation sequence. In **vitro** transcription and translation assay of this avian cDNA followed by radioimmunopptn. assay using a murine C/EBPγ antiserum indicates that this non-optimal initiation codon is used to express a 22-kDa **DNA-binding protein** .

L12 ANSWER 12 OF 44 CA COPYRIGHT 2002 ACS
TI Identification of p53 genetic suppressor elements which confer resistance to cisplatin
AU Gallagher, W. M.; Cairney, M.; Schott, B.; Roninson, I. B.; Brown, R.
SO Oncogene (1997), 14(2), 185-193
CODEN: ONCNES; ISSN: 0950-9232
PY 1997
AB Loss of p53 function is associated with the acquisition of cisplatin resistance in the human ovarian adenocarcinoma A2780 cell line. Selection for cisplatin resistance of A2780 cells was used to isolate genetic suppressor elements (GSEs) from a retroviral **library** expressing random fragments of human or murine TP53 cDNA. Six GSEs were identified, encoding either dominant neg. mutant peptides or antisense RNA mols. which corresponded to various regions within the TP53 gene. Both types of GSE induced cisplatin resistance when introduced individually into A2780 cells. Expression of antisense GSEs led to decreased intracellular levels of p53 protein. One sense GSE induced loss of p53-mediated activities such as DNA damage induced cell cycle arrest and apoptosis. A synthetic

peptide, representing the predicted amino acid sequence of this GSE, conferred resistance to cisplatin when introduced into A2780 cells and inhibited the sequence specific **DNA binding** activity of p53 **protein** in **vitro**. Overall, these results directly indicate that inactivation of p53 function confers cisplatin resistance in these human ovarian tumor cells. We have identified short structural domains of p53 which are capable of independent functional interactions and highlighted the efficacy of this approach to discriminate biol. active GSEs from a random fragment **library**.

L12 ANSWER 13 OF 44 CA COPYRIGHT 2002 ACS
TI Human telomeric binding proteins recognizing single and double stranded DNA
AU Matsuo, Ken-Ich; Yamada, Yuji; Izumi, Hiroto; Kuwano, Michihiko; Kohno, Kimitoshi
SO International Journal of Oncology (1996), 9(6), 1201-1205
CODEN: IJONES; ISSN: 1019-6439
PY 1996
AB Telomeres of human chromosomes consist of a repeated TTAGGG sequence, and at the terminus of this repeat sequence, the 3' strand is longer than the 5' strand. In this study, we characterized single and double stranded telomere-binding proteins (ssTBPs and dsTBPs) by gel mobility shift and South-Western blotting assays. At least two protein components with mol. wts. of 29 and 33 kDa were bound to a single stranded telomeric sequence, and two proteins with mol. wts. of about 44 kDa and 70 kDa were bound to a double stranded telomeric sequence. A competition assay demonstrated that the binding properties of ssTBPs and dsTBPs were specific to the telomeric sequence. We further cloned a ssTBP cDNA (ssTBP-1) by screening a λ-gt11 expression **library** and identified ssTBP-1 as a human heterogeneous nuclear ribonucleoprotein (hnRNP) A1 on the basis of cDNA sequence. We also found that the expression of the hnRNP A1 gene significantly decreased during in **vitro** passage of human microvascular endothelial cells.

L12 ANSWER 14 OF 44 CA COPYRIGHT 2002 ACS
TI Novel members of a family of AT hook-containing DNA-binding proteins from rice are identified through their in **vitro** interaction with consensus target sites of plant and animal homeodomain proteins
AU Meijer, Annemarie H.; van Dijk, Erwin L.; Hoge, J. Harry C.
SO Plant Molecular Biology (1996), 31(3), 607-618
CODEN: PMBIDB; ISSN: 0167-4412
PY 1996
AB The AT hook is an AT-rich DNA-binding domain that occurs three times in mammalian high-mobility-group I/Y chromosomal proteins and has recently also been identified in DNA-binding proteins from plants. We unexpectedly isolated three rice cDNA clones encoding AT hook-containing proteins in an attempt to isolate homeobox cDNA clones by south-western screening of an expression **library** with known binding sites for Arabidopsis and animal homeodomain proteins. One of these clones (Os-PF1) has previously been identified due to the binding of its encoded protein to PE1, a cis-acting element from the oat phytochrome promoter. The other two clones represent newly described cDNA clones, designated Os-AT1 and Os-AT2. The Os-AT1 and Os-AT2 proteins were found to have the same specificities as Os-PF1 with respect to in **vitro** binding of

wild-type and mutant PE1 versions. However, all three proteins appeared to bind much stronger in south-western assays to two of the rather AT-rich sequences used in our screening than to the PE1 element. In none of the AT hook proteins clear homologies to transcriptional activation domains could be identified, but the N-terminal regions of Os-AT1 and Os-PF1 were found to show similarity to histone H1 chromosomal proteins. Given their structural characteristics it is conceivable that the rice AT hook proteins bind to gene promoter regions as accessory proteins that may alter the accessibility of chromatin to other nuclear factors. Their predominant expression in young and meristematic tissues suggests that the presence of the AT hook proteins may affect the expression of genes that determine the differentiation status of cells.

L12 ANSWER 15 OF 44 CA COPYRIGHT 2002 ACS
TI GRIP1, a novel mouse protein that serves as a transcriptional coactivator in yeast for the hormone binding domains of steroid receptors
AU Hong, Heng; Kohli, Kulwant; Trivedi, Alpha; Johnson, Deborah L.; Stallcup, Michael R.
SO Proceedings of the National Academy of Sciences of the United States of America (1996), 93(10), 4948-4952
CODEN: PNASA6; ISSN: 0027-8424
PY 1996
AB The yeast two-hybrid system was used to isolate a clone from a 17-day-old mouse embryo cDNA **library** that codes for a novel 812-aa long protein fragment, glucocorticoid receptor-interacting protein 1 (GRIP1), that can interact with the hormone binding domain (HBD) of the glucocorticoid receptor. In the yeast two-hybrid system and in **vitro**, GRIP1 interacted with the HBDs of the glucocorticoid, estrogen, and androgen receptors in a hormone-regulated manner. When fused to the **DNA binding** domain of a heterologous **protein**, the GRIP1 fragment activated a reporter gene containing a suitable enhancer site in yeast cells and in mammalian cells, indicating that GRIP1 contains a transcriptional activation domain. Overexpression of the GRIP1 fragment in mammalian cells interfered with hormone-regulated expression of mouse mammary tumor virus-chloramphenicol acetyltransferase gene and constitutive expression of cytomegalovirus-β-galactosidase reporter gene, but not constitutive expression from a tRNA gene promoter. This selective squelching activity suggests that GRIP1 can interact with an essential component of the RNA polymerase II transcription machinery. Finally, while a steroid receptor HBD fused with a GAL4 DNA binding domain did not, by itself, activate transcription of a reporter gene in yeast, coexpression of this fusion protein with GRIP1 strongly activated the reporter gene. Thus, in yeast, GRIP1 can serve as a coactivator, potentiating the transactivation functions in steroid receptor HBDs, possibly by acting as a bridge between HBDs of the receptors and the basal transcription machinery.

L12 ANSWER 16 OF 44 CA COPYRIGHT 2002 ACS
TI Isolation of two novel myb-like genes from Arabidopsis and studies on the DNA-binding properties of their products
AU Li, Song Feng; Parish, Roger W.
SO Plant Journal (1995), 8(6), 963-72
CODEN: PLJUED; ISSN: 0960-7412
PY 1995

AB Two novel myb-like genes (atmyb6 and atmyb7) were isolated from an Arabidopsis thaliana cDNA **library**. The entire proteins or the Myb domains encoded by the genes were expressed as fusion proteins in Escherichia coli. The DNA-binding domain of the murine c-Myb was also expressed in the same way for use in comparative studies. The fusion proteins were examined for their DNA-binding activity using the animal c-Myb DNA-binding site (MBS) and the binding site of the maize P gene product (PBS). The Myb domain of Atmyb6 bound to PBS more efficiently than to MBS. Complete Atmyb6 and Atmyb7 proteins preferentially bound to PBS but not MBS. This suggests that the in **vitro** binding consensus sequences for both Atmyb6 and Atmyb7 are similar to PBS. The binding of the Myb domain of Atmyb6 to both PBS and MBS raises the possibility that the protein recognizes multiple sequences in vivo. The third α-helix and three adjacent amino acids in the third repeat (R3) of c-Myb were replaced with the analogous sequence of Atmyb6 to create a chimeric Myb protein. This chimeric protein bound to PBS with a low affinity but failed to bind to MBS. Thus the binding pattern of the chimeric Myb protein is similar to that of the Atmyb6. This result suggests that the last 20 amino acids in the R3 repeat of Atmyb6 play a major role in DNA-binding.

L12 ANSWER 17 OF 44 CA COPYRIGHT 2002 ACS
TI Cloning and characterization of a novel cellular protein, TDP-43, that binds to human immunodeficiency virus type 1 TAR DNA sequence motifs
AU Ou, S.-H. Ignatius; Wu, Foon; Harrich, David; Garcia-Martinez, Leon F.; Gaynor, Richard B.
SO Journal of Virology (1995), 69(6), 3584-96
CODEN: JOVIAM; ISSN: 0022-538X
PY 1995
AB Human immunodeficiency virus type 1 (HIV-1) gene expression is modulated by both viral and cellular factors. A regulatory element in the HIV-1 long terminal repeat known as TAR, which extends from nucleotides -18 to +80, is critical for the activation of gene expression by the transactivator protein, Tat. RNA transcribed from TAR forms a stable stem-loop structure which serves as the binding site for both Tat and cellular factors. Although TAR RNA is critical for Tat activation, the role that TAR DNA plays in regulating HIV-1 gene expression is not clear. Several studies have demonstrated that TAR DNA can bind cellular proteins, such as UBP-1/LBP-1, which repress HIV-1 gene expression and other factors which are involved in the generation of short, nonprocessive transcripts. In an attempt to characterize addnl. cellular factors that bind to TAR DNA, a λgt11 expression cloning strategy involving the use of a portion of TAR DNA extending from -18 to +28 to probe a HeLa cDNA **library** was used. We identified a cDNA, designated TAR **DNA-binding protein** (TDP-43), which encodes a cellular factor of 43 kDa that binds specifically to pyrimidine-rich motifs in TAR. Antibody to TDP-43 was used in gel retardation assays to demonstrate that endogenous TDP-43, present in HeLa nuclear extract, also bound to TAR DNA. Although TDP-43 bound strongly to double-stranded TAR DNA via its ribonucleoprotein protein-binding motifs, it did not bind to TAR RNA extending from +1 to +80. To determine the function of TDP-43 in regulating HIV-1 gene expression, in **vitro** transcription anal. was performed. TDP-43 repressed in **vitro** transcription from the HIV-1 long terminal repeat in both the presence and absence of Tat, but it did not repress transcription from

other promoters such as the adenovirus major late promoter. In addition, transfection of a vector which expressed TDP-43 resulted in the repression of gene expression from an HIV-1 provirus. These results indicate that TDP-43 is capable of modulating both in **vitro** and in vivo HIV-1 gene expression by either altering or blocking the assembly of transcription complexes that are capable of responding to Tat.

L12 ANSWER 18 OF 44 CA COPYRIGHT 2002 ACS
TI Gene isolation by screening λgt11 expression **libraries** with DNA-binding site probes
AU Kalionis, Bill
SO Methods in Molecular Biology (Totowa, New Jersey) (1995), 37(In Vitro Transcription and Translation Protocols), 393-407
CODEN: MMBIED; ISSN: 1064-3745
PY 1995
AB A review with 11 refs. A fundamental goal of gene anal. is to determine what factors regulate the temporal and spatial expression of the gene of interest. This type of anal. requires the identification of the promoter region of the gene, characterization of the specific DNA sequences that regulate the expression of the gene, and the determination of the DNa-binding factors that recognize these sequences. The first 2 requirements can be met by routine in **vitro** mol. biol. techniques, which allow the DNA-binding sequence to be defined to a short DNA sequence, but isolating the specific DNa-binding factors that regulate the transcription of the gene, has proven to be problematic. One common strategy is to isolate the DNA-binding factor from complex mixts. of proteins and then to us a "reverse genetics" approach to clone the gene that encodes the factor. A more direct approach is to screen an expression **library** with a short radioactively labeled DNA sequence defined in **vitro** as a binding site for the factor. The vector most commonly used for **library** construction is λgt11, where cDNA inserts are cloned into a unique EcoRI site near the C-terminal end of the coding region of the lacZ gene. The β-galactosidase fusion protein can be induced to high levels in the presence of the inducer IPTG. The aim of this review is to provide a basic protocol, a set of notes relating to tech. detail, and a troubleshooting guide to assist in problem solving.

L12 ANSWER 19 OF 44 CA COPYRIGHT 2002 ACS
TI Identification of nuclear factors that bind to the mouse tyrosinase gene regulatory region
AU Sato, Shigeru; Miura, Hirohito; Yamamoto, Hiroaki; Takeuchi, Takuji
SO Pigment Cell Research (1994), 7(5), 279-84
CODEN: PCREEA; ISSN: 0893-5785
PY 1994
AB Several nuclear factors that interact with sequences in the 5' flanking region of the mouse tyrosinase gene were identified using band shift and methylation interference assays. One of these factors bind to an AT-rich sequence, TATCAATTAG, located at -183 base pairs upstream of the transcription start site. To isolate cDNA clone encoding this **DNA binding protein**, we have screened a λgt11 cDNA expression **library** prepared from mouse melanocyte cell line with a labeled oligonucleotide probe containing its binding site. Complementary DNA clones encoding mouse high mobility group protein HMG-I and its isoform HMG-Y were obtained. HMG-I(Y) is a low mol. size, basic nuclear protein that binds specifically to AT-rich region of double-stranded DNA in

vitro. In Northern blot anal. the level of HMG-I(Y) mRNA expression did not correlate with that of tyrosinase or TRP-1. Although the amount of HMG-I(Y) transcripts has no apparent influence on the mouse tyrosinase gene expression, it is possible that HMG-I(Y) binds to the 5' flanking sequence of the tyrosinase gene as an auxiliary factor, and facilitates the binding and activity of other transcription factors.

L12 ANSWER 20 OF 44 CA COPYRIGHT 2002 ACS
TI The murine nucleolin protein is an inducible **DNA** and ATP **binding protein** which is readily detected in nuclear extracts of lipopolysaccharide-treated splenocytes
AU Miranda, Gustavo A.; Chokler, Ilona; Aguilera, Renato J.
SO Experimental Cell Research (1995), 217(2), 294-308
CODEN: ECREAL; ISSN: 0014-4827
PY 1995
AB A 100-kDa **DNA binding protein** was dramatically up-regulated upon the mitogenic stimulation of murine splenocytes with bacterial lipopolysaccharide (LPS). The induced **DNA binding protein** was also found to exhibit moderate binding specificity for the Ig isotype switch DNA repeats. Furthermore, the induction of the 100-kDa protein by LPS was mediated by both an increase in the protein's stability and an increase in the synthesis of the protein. In **vitro** phosphorylation expts. revealed that the 100-kDa **DNA binding protein** was one of the most heavily phosphorylated proteins in both lymphoid and nonlymphoid nuclear exts. Although this in **vitro** phosphorylation initially appeared to be mediated by a potent nuclear kinase activity, it was later determined that a significant part of the detected labeling was due to the direct binding of ATP by the 100-kDa protein. Antibodies raised to the 100-kDa **DNA binding protein** were used to isolate cDNA clones from a lymphocyte cDNA λgt11 expression **library**. Nucleotide sequence anal. revealed that the cloned cDNAs were identical to the mouse nucleolin gene. The β-galactosidase fusion proteins (encoded by exons 3-14 of nucleolin) and a more severely truncated 45-kDa protein (encoded by exons 5-14 of nucleolin) were both found to bind strongly to DNA and ATP. Furthermore, the strength of DNA binding was highly dependent on the overall dG content of the DNA probes. The expts. also revealed that apart from binding ATP and G-rich DNA, nucleolin directly bound GTP, dATP, and dGTP, but not dCTP, dTTP, or dUTP. Computer anal. revealed that the putative ATP binding domains appear to fall within two of the phylogenetically conserved RNA binding domains of nucleolin.

L12 ANSWER 21 OF 44 CA COPYRIGHT 2002 ACS
TI Hepatitis B virus X protein interacts with a probable cellular DNA repair protein
AU Lee, Teh-Hsiu; Elledge, Stephen J.; Butel, Janet S.
SO Journal of Virology (1995), 69(2), 1107-14
CODEN: JOVIAM; ISSN: 0022-538X
PY 1995
AB The mechanism of action of hepatitis B virus (HBV) X protein in transcriptional transactivation and in tumorigenesis remains obscure. The authors have used the yeast two-hybrid system to identify a cellular protein that can interact with HBV X protein. This protein, designated X-associated protein 1 (XAP-1), is a human homolog of the UV-damaged **DNA-binding protein** (UV-DDB) recovered from a monkey cell cDNA **library**. UV-DDB is presumed to be involved in

DNA repair. The interaction between X protein and XAP-1 protein was verified by immunopptn. of yeast cell lysates expressing both proteins and by in **vitro** mixing with X protein expressed as a glutathione S-transferase fusion protein and XAP-1 protein either in HeLa cell exts. or synthesized by in **vitro** translation. The authors speculate that the interaction of X protein with a DNA repair protein may recruit cellular proteins to repair the partially double-stranded HBV genome or may modify cellular transcription processes. An effect on the cellular DNA repair system may explain a cofactor role for HBV in liver cancer development.

L12 ANSWER 22 OF 44 CA COPYRIGHT 2002 ACS
TI Cloning of a **DNA binding protein** that is a tyrosine kinase substrate and recognizes an upstream initiator-like sequence in the promoter of the preprodynorphin gene
AU Gu, J.; Ren, K.; Dubner, R.; Iadarola, M. J.
SO Molecular Brain Research (1994), 24(1-4), 77-88
CODEN: MBREE4; ISSN: 0169-328X
PY 1994
AB A 90 bp fragment prepared from the promoter region of the rat preprodynorphin gene formed a complex with rat brain nuclear exts. as assessed by gel mobility shift assays. An 8 base pair sequence, CACTCTCC, termed upstream regulatory element (URE), was identified within this fragment as a binding site by DNase 1 footprint anal. and gel mobility shift assays with synthetic oligonucleotides. The URE is a consensus sequence for a transcription initiator (Inr) element although in the preprodynorphin promoter it is located upstream at -208 and overlaps a region conserved between rat and human promoters. A unique 310 amino acid protein (UreB1) that specifically bound the URE was cloned from a rat brain cDNA **library** using the URE-containing oligonucleotide. Recombinantly expressed, affinity purified UreB1 protein retains specific binding to the URE oligonucleotide. UreB1 contains a tyrosine kinase phosphorylation consensus and binding is enhanced following phosphorylation with the p43v-abl tyrosine kinase. The UreB1 tyrosine phosphoprotein increases transcription in **vitro**, consistent with a pos. transcriptional regulatory function. UreB1 transcripts are well expressed in subsets of neurons in multiple brain areas suggesting that, in addition to regulation of the preprodynorphin gene, it may have a more generalized role in gene transcription.

L12 ANSWER 23 OF 44 CA COPYRIGHT 2002 ACS
TI Isolation and characterization of two Saccharomyces cerevisiae genes that encode proteins that bind to (TG1-3)n single strand telomeric DNA in **vitro**
AU Lin, Jing-Jer; Zakian, Virginia A.
SO Nucleic Acids Research (1994), 22(23), 4906-13
CODEN: NARHAD; ISSN: 0305-1048
PY 1994
AB By screening λgt11 **libraries** with a radiolabeled (TG1-3)n oligonucleotide, two Saccharomyces cerevisiae genes were identified that encode polypeptides that recognize the single-stranded telomeric repeat sequence (TG1-3)n. The first gene, NSR1, a previously identified gene, encodes a protein involved in rRNA maturation and possibly in transport of proteins into the nucleus. The second gene, GBP2 (G-strand Binding Protein), is an anonymous open reading frame from chromosome III. These two genes contain RNA recognition motifs (RRMs) that are found in proteins

that interact with RNA. Both Nsr1p and Gbp2p bind specifically to yeast single strand (TG1-3)n DNA in **vitro**. To test whether these two proteins associate with telomeres in vivo, strains were constructed in which one or both of these genes were either disrupted or overexpressed. None of these alterations affected telomere length or telomere position effect. The potential role of these two (TG1-3)n binding proteins is discussed.

L12 ANSWER 24 OF 44 CA COPYRIGHT 2002 ACS
TI Isolation of human DNA-unwinding elements as sites of DNA polymerase α/primase entry
AU Pack, Robert A.; Tsurimoto, Toshiki
SO Gene (1994), 148(2), 277-84
CODEN: GENED6; ISSN: 0378-1119
PY 1994
AB Human DNA **libraries** were screened for DNA synthesis activity in **vitro** using purified DNA polymerase α/primase and a viral DNA helicase (simian virus 40 large tumor antigen). Three clones exhibited a high activity distinguishable from the rest. The DNA synthesis was dependent on neg. supertwisting and initiated at a unique region in the human DNA insert. Functional subclone DNA fragments which could be shortened to less than 1kb are located in the initiation region. Binding with a single-stranded **DNA-binding protein** and digestion with nuclease P1 demonstrated that these DNAs have a highly single-stranded nature at a certain site in a closed circular plasmid. The minimal functional sequences coincide with the single-stranded region and contain a characteristic dinucleotide repeat sequence. These repeats have an extremely low free energy for DNA strand separation and are defined as DNA-unwinding elements, which are frequently observed at regions flanking replication origins in Escherichia coli and Saccharomyces cerevisiae chromosomes. We suggest that such a repeating sequence would have an important role during initiation of DNA replication and function as a site to recruit replication proteins.

L12 ANSWER 25 OF 44 CA COPYRIGHT 2002 ACS
TI Isolation and characterization of MRF-1, a brain-derived **DNA-binding protein** with a capacity to regulate expression of myelin basic protein gene
AU Haque, Nasreen S.; Buchberg, Arthur M.; Khalili, Kamel
SO Journal of Biological Chemistry (1994), 269(49), 31149-56
CODEN: JBCHA3; ISSN: 0021-9258
PY 1994
AB The 5'-flanking region of the myelin basic protein (MBP) contains several regulatory elements that differentially contribute to the cell type-specific transcription of MBP in cells derived from the central nervous system. The distal regulatory element, termed MB3, had previously been shown to have characteristics of a cell type-specific enhancer element and bind to multiple brain-derived nuclear proteins in **vitro**. We now report the isolation of a recombinant cDNA clone, named myelin regulatory factor-1 (MRF-1) from a mouse brain expression **library** that encodes a novel protein which interacts with the MB3 domain. Computer-assisted anal. of MRF-1 revealed substantial sequence homol. in the central and the COOH-terminal regions of this protein with the previously identified splicing factor SC35. Co-transfection studies indicated that MRF-1 increases transcription of the MBP promoter in glial cells and that this activation requires an intact MRF-1 binding site

within the MB3 region. MRF-1 cDNA hybridized to three RNA species 1.8, 2.5, and 3.0 kilobases which are expressed in all tissues analyzed. The gene encoding MRF-1 is located on the distal half of mouse chromosome 11 in a region where the human homolog would be predicted to reside on human chromosome 17.

L12 ANSWER 26 OF 44 CA COPYRIGHT 2002 ACS
TI Human protein NEFA, a novel **DNA binding** /EF-hand/leucine zipper **protein**. Molecular cloning and sequence analysis of the cDNA, isolation and characterization of the protein
AU Barnikol-Watanabe, Shitsu; Gross, Nikola A.; Goetz, Hilde; Henkel, Thomas;
Karabinos, Anton; Kratzin, Hartmut; Barnikol, Heinz Ulrich; Hilschmann, Norbert
SO Biological Chemistry Hoppe-Seyler (1994), 375(8), 497-512
CODEN: BCHSEI; ISSN: 0177-3593
PY 1994
AB The cDNA **libraries** constructed from the human acute lymphoblastic leukemia cell line KM3 in the expression vector λgt11, were screened with the anti-CALLA (common acute lymphoblastic leukemia antigen) mAb (monoclonal antibody) J5. The selected J5-pos. clone I containing a partial cDNA insert was isolated and
sequenced. For completing the cDNA sequence the cDNA **libraries** were further screened by hybridization with the DIG (digoxigenin)-labeled DNA probe derived from clone I, the 5'-end region was analyzed by 5'-RACE (rapid amplification of cDNA ends) using a sequence specific primer. In total a 1639 bp cDNA sequence was determined The cDNA sequence contains a 1260
bp open reading frame and the untranslated 3'- and 5'-end sides. The 420 residue amino acid sequence, deduced from the cDNA sequence, unexpectedly differs fundamentally from CALLA (CD10) although clones I and II were J5-pos. in immuno screening. The mature protein corresponding to the cDNA
was isolated and characterized from the KM3 cells using polyclonal antisera raised against the in **vitro** expressed polypeptide from clone I. The protein is expressed on plasma membrane, in cytosol and is secreted into culture medium, its relative mol. mass was determined to be 55
kDa on SDS-PAGE. The deduced amino acid sequence from cDNA was confirmed by peptide sequences. The new protein contains a basic amino acid rich putative DNA binding domain (b) with a potential nuclear targeting signal,
two helix-loop-helix (HLH) motif regions, concurrently EF-hand motifs, an acidic amino acid rich region (a) between the EF-hands, and a leucine zipper (Z) motif. This **DNA binding protein** therefore is characterized by a linked motif "b/HLH/a/HLH/Z". The protein
was designated NEFA: DNA binding/EF-hand/acidic amino acid rich region.

L12 ANSWER 27 OF 44 CA COPYRIGHT 2002 ACS
TI A universal target sequence is bound in **vitro** by diverse homeodomains
AU Kalionis, Bill; O'Farrell, Patrick H.
SO Mechanisms of Development (1993), 43(1), 57-70
CODEN: MEDVE6; ISSN: 0925-4773
PY 1993
AB To determine the number of DNA binding proteins capable of binding a consensus
Engrailed binding site, this consensus sequence was used to screen a

library of Drosophila cDNA clones in a bacteriophage expression vector. The authors retrieved clones encoding 20 distinct DNA binding domains, 17 of which are homeodomains. Binding to a variety of oligonucleotides confirms the related sequence specificity of the retrieved binding domains. Nonetheless, the homeodomains have remarkably diverse amino acid sequences. The authors conclude that during the evolutionary divergence of homeodomains, the specificity of DNA binding has been much more highly conserved than the amino acid sequence.

L12 ANSWER 28 OF 44 CA COPYRIGHT 2002 ACS
TI The genes for the PUR proteins and their use in the control of replication
IN Johnson, Edward M.; Bergemann, Andrew D.
SO PCT Int. Appl., 96 pp.
CODEN: PIXXD2
PY 1994
1996
1995
AB Genes for the PUR proteins are cloned and expressed for use in anal. and inhibition of PUR activity. The PUR proteins bind specifically to single stranded DNA in regions that coincide with eukaryotic origin of replication indicating a role for the proteins in the regulation of DNA replication. Inhibitors of PUR activity of PUR activity may be used to treat hyperproliferative diseases such as cancer. A stably bent sequence near the c-myc gene was identified and a protein was shown to specifically bind to the bend of the element. This was shown to be due to binding to a guanosine-rich segment in the bent region with the protein showing a higher affinity for the single-stranded sequence than for the double-stranded. A cDNA was cloned by screening a human fetal liver **library** in λgt11 by screening for binding of probes containing the binding site. The fusion of the PUR protein and β-galactosidase from the λgt11 clone bound the binding site as shown by gel retardation assays. The protein bound to the unphosphorylated retinoblastoma protein in **vitro** with an affinity comparable to that of the SV40 large T antigen.

L12 ANSWER 29 OF 44 CA COPYRIGHT 2002 ACS
TI Mapping of the 70 kDa, 34 kDa, and 11 kDa subunit genes of the human multimeric single-stranded **DNA binding protein** (hSSB/RPA) to chromosome bands 17p13, 1p35-p36.1, and 7p21-p22
AU Ozawa, Kazuo; Dean, Frank B.; Chen, Mei; Lee, Suk Hee; Shiratori, Akiko; Murakami, Yasufumi; Sakakura, Teruyo; Hurwitz, Jerard; Eki, Toshihiko
SO Cell Structure and Function (1993), 18(4), 221-30
CODEN: CSFUDY; ISSN: 0386-7196
PY 1993
AB Human single-stranded **DNA-binding protein** (hSSB/RPA) is a multimeric single-stranded **DNA binding protein** consisting of 3 subunits of 70 kDa, 34 kDa, and 11 kDa. Human SSB was isolated from HeLa cells as an essential factor for the in **vitro** replication of simian virus 40 DNA. The authors and others have isolated and sequenced cDNAs for each subunit of the SSB. The chromosome on which each gene is located was determined through the anal. of a panel of human/hamster somatic cell hybrids using the polymerase chain reaction with pairs of synthetic oligonucleotide primers from the 3'-untranslated sequences of the genes. Genomic clones for each gene were isolated from a genomic cosmid **library** prepared from human

lymphoblastoid cells. Using those clones as probes, fluorescence in situ hybridization to human metaphase chromosomes mapped the 70-kDa subunit gene to 17p13, the 34-kDa subunit gene to 1p35-p36.1, and the 11-kDa subunit gene to 7p21-p22. Since hSSB participates in replication, recombination, and repair of DNA, the phys. mapping of hSSB genes may aid in the identification of human hereditary diseases associated with aberrant DNA reactions caused by genetic alterations of the hSSB.

L12 ANSWER 30 OF 44 CA COPYRIGHT 2002 ACS
TI Anabaena sp. strain PCC 7120 bifA gene encoding a sequence-specific **DNA-binding protein** cloned by in vivo transcriptional interference selection
AU Wei, Tai Fen; Ramasubramanian, T. S.; Pu, Frances; Golden, James W.
SO Journal of Bacteriology (1993), 175(13), 4025-35
CODEN: JOBAAY; ISSN: 0021-9193
PY 1993
AB VF1 is a **DNA-binding protein** from the cyanobacterium Anabaena sp. strain PCC 7120. VF1 was originally identified on the basis of its binding affinity to the upstream region of xisA, which encodes a heterocyst-specific site-specific recombinase. VF1 also binds to the glnA, rbcL, and nifH promoters in **vitro**, suggesting that VF1 interacts with genes expressed in both vegetative cells and heterocysts. The role of VF1 in regulating gene expression in PCC 7120 is unknown. As a step towards the goal of understanding the role of VF1 in regulating gene expression, the bifA gene was cloned by using a genetic selection strategy. BifA encodes a protein, BifA, that has chromatog. and DNA-binding properties indistinguishable from those of VF1. The cloning strategy was based on a transcriptional interference assay in which a strong synthetic promoter, conII, interferes with the expression of an aadA gene, which provides resistance to spectinomycin and streptomycin (S. J. Elledge, P. Sugiono, L. Guarente, and R. W. Davis, 1989). A selection plasmid, pAM994, which has the conII promoter neg. regulated by a VF1-binding site, was used to enrich for VF1-producing clones from an expression **library** containing PCC 7120 DNA fragments. Mobility shift assays were used to identify a 672-bp open reading frame that encoded VF1-like binding activity. The deduced BifA amino acid sequence shows 77% identity to NtcA, which is a global regulator involved in nitrogen control in Synechococcus sp. strain PCC 7942. Both BifA and NtcA belong to the cAMP receptor protein (CRP) family of prokaryotic regulatory proteins. Genes similar to envM, hisB, and ORF60-5 were found near the bifA gene.

L12 ANSWER 31 OF 44 CA COPYRIGHT 2002 ACS
TI Oxytricha telomere-binding protein: separable DNA-binding and dimerization domains of the α-subunit
AU Fang, Guowei; Gray, John T.; Cech, Thomas R.
SO Genes & Development (1993), 7(5), 870-82
CODEN: GEDEEP; ISSN: 0890-9369
PY 1993
AB A telomere-binding protein heterodimer of 56-kD (α) and 41-kD (β) subunits binds to the single-stranded (T4G4)2 terminus of each Oxytricha nova macronuclear DNA mol. The α-subunit by itself binds to telomeric DNA. The β-subunit alone does not bind to DNA specifically but interacts with the α-subunit to form a very stable ternary complex. The formation of α-β-DNA ternary complex is extremely cooperative. Furthermore, the binary complex (α-DNA) has

a dissociation half-life of much less than 1 min; addition of the β-subunit increases the half-life to .apprx.100 h. **Libraries** of plasmids with random deletions of the open reading frame for the α-subunit were introduced into Escherichia coli, and exts. were subsequently checked for both protein expression and DNA-binding activity with or without added β-subunit. The α-subunit was found to contain two structurally separable domains with distinct functions. The amino-terminal two-thirds is necessary and sufficient for sequence-specific DNA binding. The carboxy-terminal one-third is responsible for α/β-subunit interactions. When expressed sep. in E. coli, purified, and mixed together, these two domains reconstitute the activity of the wild-type α-subunit (trans-complementation in **vitro**). The amino-terminal two-thirds of the β-subunit is necessary and sufficient both for α/β-subunit interactions and for ternary complex formation. Thus, the α-subunit of the telomere-binding protein, like many transcription factors, has separable **DNA-binding** and **protein-protein** interaction domains.

L12 ANSWER 32 OF 44 CA COPYRIGHT 2002 ACS
TI Cloning of Drosophila transcription factor Adf-1 reveals homology to Myb oncoproteins
AU England, Bruce P.; Admon, Arie; Tjian, Robert
SO Proceedings of the National Academy of Sciences of the United States of America (1992), 89(2), 683-7
CODEN: PNASA6; ISSN: 0027-8424
PY 1992
AB The Drosophila sequence-specific **DNA binding protein**, Adf-1, is capable of activating transcription of the alc. dehydrogenase gene, Adh, and is implicated in the transcriptional control of other developmentally regulated genes. The cDNA encoding Adf-1 was cloned by generating specific DNA probes deduced from partial amino acid sequence of the protein. Several cDNA clones encoding an extended open reading frame were isolated from a phage λ **library**. The complete amino acid sequence of Adf-1 deduced from the longest cDNA reveals structural similarities to the putative helix-turn-helix DNA binding motif of Myb and Myb-related proteins. DNA sequence anal. of genomic clones and Northern blot anal. of mRNA suggest that Adf-1 is a single-copy gene encoding a 1.9-kb transcript. Purified recombinant Adf-1 expressed in Escherichia coli binds specifically to Adf-1 recognition sites and activates transcription of a synthetic Adh promoter in **vitro** in a manner indistinguishable from the protein purified from Drosophila. Temporally staged Drosophila embryos immunochem. stained with affinity-purified anti-Adf-1 antibodies indicate that Adf-1 protein is not detectable in very early embryos and does not appear to be maternally inherited. During later stages of embryogenesis, Adf-1 appears to be expressed in the nucleus of most somatic cells in the embryo with possibly higher concns. found in some tissues.

L12 ANSWER 33 OF 44 CA COPYRIGHT 2002 ACS
TI An essential yeast gene encoding a TTAGGG repeat-binding protein
AU Brigati, Claudio; Kurtz, Stephen; Balderes, Dina; Vidali, Giorgio; Shore, David

SO Molecular and Cellular Biology (1993), 13(2), 1306-14
CODEN: MCEBD4; ISSN: 0270-7306
PY 1993
AB A yeast gene encoding a **DNA-binding protein** that recognizes the telomeric repeat sequence TTAGGG found in multicellular eukaryotes was identified by screening a λgt11 expression **library** with a radiolabeled TTAGGG multimer. This gene, which the authors refer to as TBF1 (TTAGGG repeat-binding factor 1), encodes a polypeptide with a predicted mol. mass of 63 kDa. The TBF1 protein, produced in **vitro** by transcription and translation of the cloned gene, binds to (TTAGGG)n probes and to a yeast telomeric junction sequence that contains 2 copies of the sequence TTAGGG separated by 5 bp. TBF1 appears to be identical to a previously described yeast TTAGGG-repeat binding activity called TBFα. TBF1 produced in **vitro** yields protein-DNA complexes with (TTAGGG)n probes that have mobilities on native polyacrylamide gels identical to those produced by partially purified TBFα from yeast cells. Furthermore, when exts. are prepared from a strain containing a TBF1 gene with an antigen tag, the authors find that the antigen copurifies with the predominant (TTAGGG)n-binding activity in the exts. The DNA sequence of TBF1 was determined The predicted protein sequence suggests that TBF1 may contain a nucleotide-binding domain, but no significant similarities to any other known proteins were identified, nor was an obvious DNA-binding motif apparent. Diploid cells heterozygous for a tbf1::URA3 insertion mutation are viable but upon sporulation give rise to tetrads with only two viable spores, both of which are Ura-, indicating that the TBF1 gene is essential for growth. Possible functions of TBF1 (TFBα) are discussed in light of these new results.

L12 ANSWER 34 OF 44 CA COPYRIGHT 2002 ACS
TI Binding of a protein tyrosine phosphatase to DNA through its carboxy-terminal noncatalytic domain
AU Radha, Vegesna; Kamatkar, Shubhangi; Swarup, Ghanshyam
SO Biochemistry (1993), 32(9), 2194-201
CODEN: BICHAW; ISSN: 0006-2960
PY 1993
AB The noncatalytic domain of a non-receptor-type protein-tyrosine phosphatase (the T-cell phosphatase or PTP-S) isolated from a rat spleen cDNA **library** shows homol. with the basic domains of transcription factors Fos and Jun (Swarup, G. et al., 1991). This phosphatase was expressed in Escherichia coli under the control of T7 promoter. The PTP-S gene product expressed in E. coli shows protein-tyrosine phosphatase activity and binds to DNA at pH 7.4 as determined by DNA affinity chromatog., Southwestern blotting, and gel retardation methods. The carboxy-terminal region of this phosphatase was fused with glutathione S-transferase by constructing expression vectors. Expts. using fusion proteins with glutathione S-transferase suggest that the carboxy-terminal 57 amino acids of PTP-S are sufficient for DNA binding. Deletion of the C-terminal 57 amino acids of PTP-S protein abolished its DNA binding property, as determined by Southwestern blotting, but not its enzymic activity. This suggests that the C-terminal 57 amino acids are essential for the **DNA binding** function of this **protein** but not for its enzymic activity. Another non-receptor-type protein-tyrosine phosphatase, PTP-1, when expressed in

enzymically active form in E. coli did not bind to DNA. These results suggest that a nontransmembrane protein-tyrosine phosphatase, PTP-S, binds to DNA in **vitro** through its carboxy-terminal noncatalytic region.

L12 ANSWER 35 OF 44 CA COPYRIGHT 2002 ACS
TI The isolation of transcription factors from λgt11 cDNA expression **libraries**: human steroid 5α-reductase 1 has sequence-specific DNA binding activity
AU Gaston, Kevin; Fried, Mike
SO Nucleic Acids Research (1992), 20(23), 6297-301
CODEN: NARHAD; ISSN: 0305-1048
PY 1992
AB The Surf-1/Surf-2 bi-directional promoter contains binding sites for at least 3 transcription factors (Su1, Su2, and Su3). By screening a λgt11 HeLa cell cDNA expression **library** with a concatenated Su2 factor binding site, a cDNA which encodes a protein with sequence-specific DNA binding activity was isolated. Gel retardation assays showed that the cloned factor binds specifically to the Su2 factor binding site present in the human Surf-1/Surf-2 promoter but not to an Su2 site containing mutated base pairs. Co-transfection expts. demonstrated that the cloned cDNA had little or no effect on the expression of a reporter gene under the control of multiple Su2 factor binding sites. Similarly a fusion protein in which the acidic activation domain of HSV VP16 was linked to the cloned factor had no effect, implying that the factor does not function as a **DNA binding protein** in vivo. DNA sequence anal. revealed that the cloned cDNA is identical to that of human steroid 5α-reductase 1, an enzyme which converts testosterone to dihydrotestosterone. These results are discussed with respect to other putative transcription factors which have been isolated from cDNA expression **libraries** on the basis of their sequence-specific DNA binding activity.

L12 ANSWER 36 OF 44 CA COPYRIGHT 2002 ACS
TI A recombinant cDNA derived from human brain encodes a **DNA binding protein** that stimulates transcription of the human neurotropic virus JCV
AU Kerr, Douglas; Khalili, Kamel
SO Journal of Biological Chemistry (1991), 266(24), 15876-81
CODEN: JBCHA3; ISSN: 0021-9258
PY 1991
AB The human neurotropic virus JCV contains a 98-base pair repeat enhancer/promoter sequence that confers glial-specific transcription to the viral early and late promoters. The central region of this repeat, designated the B-domain, binds to a glial-derived nuclear protein that stimulates transcription of the viral promoter in **vitro**. The isolation of a recombinant cDNA clone, termed glial factor-1 (GF1), from a brain expression **library** that encodes a novel protein which interacts with the JCV B-domain is reported. Results from RNA studies indicate that the GF1 transcript is more abundant in brain than in other tissues and that the level of GF1 RNAs increases progressively during brain development. Cotransfection of the recombinant GF1 expressor plasmid with JCV promoters indicates that GF1 stimulates transcription of the JCV late promoter and to a lesser extent the JCV early promoter predominantly in cells of human glial origin. Thus, GF1 is a sequence-specific **DNA binding protein** that

may play a role in determining the glial-specific expression of JCV.

L12 ANSWER 37 OF 44 CA COPYRIGHT 2002 ACS
TI A cyclic AMP-responsive **DNA-binding protein** (CREB2) is a cellular transactivator of the bovine leukemia virus long terminal repeat
AU Willems, Luc; Kettmann, Richard; Chen, Gao; Portetelle, Daniel; Burny, Arsene; Derse, David
SO Journal of Virology (1992), 66(2), 766-72
CODEN: JOVIAM; ISSN: 0022-538X
PY 1992
AB To gain insight into the cellular regulation of bovine leukemia virus (BLV) trans activation, a lambda-gt11 cDNA **library** was constructed with mRNA isolated from a BLV-induced tumor and the recombinant proteins were screened with an oligonucleotide corresponding to the tax activation-responsive element (TAR). Two clones (called TAR-binding protein) were isolated from 750,000 lambda-gt11 plaques. The binding specificity was confirmed by Southwestern (DNA-protein) and gel retardation assays. Nucleotide sequence anal. revealed that TAR-binding protein is very similar to the CREB2 protein. It contains a leucine zipper structure required for dimerization, a basic amino acid domain, and multiple potential phosphorylation sites. A vector expressing CREB2 was transfected into D17 osteosarcoma cells. In the absence of the tax transactivator, the CREB2 protein and the cAMP-dependent protein kinase A activate the BLV long terminal repeat at a basal expression level: trans activation reached 10% of the values obtained in the presence of tax alone. These data demonstrate that CREB2 is a cellular factor able to induce BLV long terminal repeat expression in the absence of tax protein and could thus be involved in the early stages of viral infection. In addition, it was observed that in **vitro** tax-induced trans activation can be activated or inhibited by CREB2 depending on the presence or absence of protein kinase A. These data suggest that the cAMP pathway plays a role in the regulation of viral expression in BLV-infected animals.

L12 ANSWER 38 OF 44 CA COPYRIGHT 2002 ACS
TI A metal-dependent **DNA-binding protein** interacts with a constitutive element of a light-responsive promoter
AU Lam, Eric; Kano-Murakami, Yuriko; Gilmartin, Philip; Niner, Bettina; Chua, Nam Hai
SO Plant Cell (1990), 2(9), 857-66
CODEN: PLCEEW; ISSN: 1040-4651
PY 1990
AB DNase I footprinting was used to characterize nuclear factors that bind to the light-responsive promoter of pea rbcS-3A, one member of the gene family encoding the small subunit of ribulose-1,5-bisphosphate carboxylase. A sequence-specific binding activity, designated 3AF1, binds to an AT-rich sequence present at the -45 region of the rbcS-3A promoter. A tetramer of the 3AF1 binding site, designated as Box VI, can form multiple complexes with tobacco leaf and root nuclear exts. Mutations of 3 base pairs in Box VI severely reduce DNA-protein complex formation in **vitro**. The wild-type Box VI tetramer, but not the mutant tetramer, is active in transgenic tobacco plants when placed upstream of the cauliflower mosaic virus 35S promoter truncated at -90. These results correlate binding of 3AF1 to the in vivo function of Box VI. The Box VI

tetramer/35S chimeric construct confers expression in diverse cell types and organs and its activity is not dependent on light. By using the Box VI tetramer as a probe to screen a cDNA expression **library**, a putative cDNA clone was obtained for the 3AF1 DNA-binding activity. Lysogen exts. of Escherichia coli expressing the cDNA clone give sequence-specific complexes with Box VI. The deduced amino acid sequence of the protein encoded by the cDNA contains two stretches of about 100 residues that are 80% homologous. Moreover, in each of the two repeats, there is an arrangement of histidines and cysteines, which may be related to the two known types of zinc-finger motifs found in many DNA-binding proteins. Consistent with the expectation that metal coordination plays an important role in **DNA binding** by this **protein**, 1,10-phenanthroline was found to abolish the formation of DNA-protein complexes. Interestingly, the same treatment did not abolish the DNA binding activity of 3AF1 in crude nuclear exts. of tobacco. These data indicate that the nuclear 3AF1 activity is likely due to multiple DNA-binding proteins all interacting with Box VI in **vitro**. RNA gel blot anal. shows that multiple transcripts homologous to this cDNA clone are expressed in different tobacco organs.

L12 ANSWER 39 OF 44 CA COPYRIGHT 2002 ACS
TI The role of RAP1 in the regulation of the MATα locus
AU Giesman, Donnamarie; Best, Lewis; Tatchell, Kelly
SO Molecular and Cellular Biology (1991), 11(2), 1069-79
CODEN: MCEBD4; ISSN: 0270-7306
PY 1991
AB The RAP1 gene of Saccharomyces cerevisiae encodes an abundant **DNA -binding protein**, also known as GRF1, TBA, or TUF, that binds to many sites in the yeast genome in **vitro**. These sites define a consensus sequence, 5'-(A/G)(A/G)ACCCANNCA(T/C)(T/C)-3', and deletion analyses of genes that contain this sequence have implicated the involvement of RAP1 in numerous cellular processes, including gene activation and repression. The MATα locus, required for determination of the α cell type in yeast cells, contains a RAP1 binding site; this site coincides with the MATα upstream activating sequence (UAS) and is necessary for expression of the two genes encoded by the MATα locus, MATα1 and MATα2. This report shows that the MATα UAS is sufficient to activate transcription from a promoterless gene fusion of the yeast CYC1 upstream region and the lacZ gene. Constructs containing only the MATα UAS generated elevated levels of β-galactosidase activity which were indistinguishable from those of constructs containing the entire MATα intergenic region. Further, the MATα UAS has an intrinsic polarity of transcriptional activation; transcription of CYC1-lacZ was six- to sevenfold higher when the UAS was oriented in the direction normally associated with MATα2 transcription. Point mutations in the MATα UAS that reduce MATα expression three- to fivefold resulted in a bi-mating phenotype, while a mutation that reduced MATα expression still further resulted in an a-mating phenotype. Plasmids were isolated from a high-copy-number yeast **library** that suppressed the bi-mating defect of point mutations in the MATα UAS, and the most effective dosage suppressor contained the gene encoding RAP1. A temperature-sensitive rap1 mutant bi-mates at the semipermissive temperature Double mutants at rap1 and matα mate exclusively as a cells, at all temps., and do not express detectable levels of MATα RNA. These data provide evidence that the RAP1 gene product functions at the MATα UAS in vivo.

L12 ANSWER 40 OF 44 CA COPYRIGHT 2002 ACS

TI Sequence-specific DNA binding of the proto-oncoprotein ets-1 defines a transcriptional activator sequence within the long terminal repeat of the Moloney murine sarcoma virus
AU Gunther, Cathy V.; Nye, Julie A.; Bryner, Roger S.; Graves, Barbara J.
SO Genes & Development (1990), 4(4), 667-79
CODEN: GEDEEP; ISSN: 0890-9369
PY 1990
AB The ets proto-oncogene family is a group of sequence-related genes whose normal cellular function is unknown. In a study of cellular proteins involved in the transcriptional regulation of murine retroviruses in T lymphocytes, it was discovered that a member of the ets gene family encodes a sequence-specific **DNA-binding protein**. A mouse ets-1 cDNA clone was obtained by screening a mouse thymus cDNA expression **library** with a double-stranded oligonucleotide probe representing 20 bp of the Moloney murine sarcoma virus (MSV) long terminal repeat (LTR). The cDNA sequence has an 813-bp open reading frame (ORF) whose predicted amino acid sequence is 97.6% identical to the 272 C-terminal amino acids of the human ets-1 protein. The ORF was expressed in bacteria, and the 30-kDa protein product was shown to bind DNA in a sequence-specific manner by mobility-shift assays, Southwestern blot anal., and methylation interference. A mutant LTR containing 4 base-pair substitutions in the ets-1-binding site was constructed and was shown to have reduced binding in **vitro**. Transcriptional efficiency of the MSV LTR promoter containing this disrupted ets-1-binding site was compared to the activity of a wild-type promoter in mouse T lymphocytes in culture, and 15-20-fold reduction in expression of a reported gene was observed It is proposed that ets-1 functions as a transcriptional activator of mammalian type-C retroviruses and that ets-related genes constitute a new group of eukaryotic DNA-binding proteins.

L12 ANSWER 41 OF 44 CA COPYRIGHT 2002 ACS
TI DNA binding activities of three murine Jun proteins: stimulation by Fos
AU Nakabeppu, Yusaku; Ryder, Kevin; Nathans, Daniel
SO Cell (Cambridge, Mass.) (1988), 55(5), 907-15
CODEN: CELLB5; ISSN: 0092-8674
PY 1988
AB Three members of the Jun/AP-1 protein family have previously been identified in mouse cDNA **libraries**: c-Jun, Jun-B, and Jun-D. The DNA binding properties of the Jun proteins were compared by using in **vitro** translation products in gel retardation assays. Each protein was able to bind to the consensus AP-1 site (TGACTCA) and, with lower affinity, to related sequences, including the cAMP response element TGACGTCA. The relative binding to the oligonucleotides tested was similar for the different proteins. The Jun proteins formed homodimers and heterodimers with other members of the family, and they were bound to the AP-1 site as dimers. When Fos translation product was present, DNA binding by Jun increased markedly, and the DNA complex contained Fos. The C-terminal homol. region of Jun was sufficient for DNA binding, dimer formation, and interaction with Fos. The general conclusion is that c-Jun, Jun-B, and Jun-D are similar in their DNA binding properties and in their interaction with Fos. If there are functional differences between them, they are likely to involve other activities of the Jun proteins.

L12 ANSWER 42 OF 44 CA COPYRIGHT 2002 ACS
TI Purification and cloning of a **DNA binding protein** from yeast that binds to both silencer and activator elements
AU Shore, David; Nasmyth, Kim
SO Cell (Cambridge, Mass.) (1987), 51(5), 721-32
CODEN: CELLB5; ISSN: 0092-8674
PY 1987
AB A **DNA-binding protein** (RAP1, previously called SBF-E) has been shown to bind to putative regulatory sites at both yeast mating-type silencers, yet is not the product of genetically identified regulators of the silent loci. Here, the purification of RAP1 by DNA affinity chromatog., and the isolation of its gene from a λgt11 genomic **library** using antibodies raised against the protein is described. Disruption of the chromosomal copy of this gene is lethal. RAP1 protein also binds in **vitro** to the upstream activation site (UAS) of MATα and ribosomal protein genes. In addition, 2 different UAS-associated RAP1-binding sites can substitute in vivo for a silencer-binding site. Thus, RAP1 may be a transcriptional regulator that can play a role in either repression or activation of transcription, depending on the context of its binding site.

L12 ANSWER 43 OF 44 CA COPYRIGHT 2002 ACS
TI Site-specific DNA binding of nuclear factor I: effect of the spacer region
AU Gronostajski, R. M.
SO Nucleic Acids Res. (1987), 15(14), 5545-59
CODEN: NARHAD; ISSN: 0305-1048
PY 1987
AB Nuclear factor I (NFI) is a site-specific **DNA-binding protein** required for the replication of adenovirus type 2 DNA in **vitro** and in vivo. To study sequence requirements for the interaction of NFI with **DNA**, measured the **binding** of the **protein** to a variety of synthetic sites was measured. Binding sites for NFI (FIB sites) were previously shown to contain a consensus sequence composed of 2 motifs, TGG (Motif 1) and GCCAA (Motif 2), separated by a 6 or 7 bp spacer region. To assess conserved sequences in the spacer region and flanking sequences which affect NFI binding, clones were isolated from oligonucleotide **libraries** that contain the two motifs flanked by 3 degenerate nucleotides and separated by degenerate spacer regions of 6 or 7 nucleotides. With a 6 bp spacer region, a strong bias exists for a C or A residue in the first position of the spacer. Sites with a 7 bp spacer region contain a G and C or A residue at the first and second positions, resp., of the spacer, but also possess conserved residues at other positions of the site.

L12 ANSWER 44 OF 44 CA COPYRIGHT 2002 ACS
TI Filter transfer of genomic **libraries** in a state accessible to DNA-binding proteins
AU Beebee, Trevor J. C.
SO Anal. Biochem. (1987), 162(1), 242-50
CODEN: ANBCA2; ISSN: 0003-2697
PY 1987
AB A method was developed for transferring plaque DNA of λ genomic **libraries** onto 3MM filters in a state accessible to DNA-binding

proteins. DNA bound to 3MM is available to proteins as large as Escherichia coli RNA polymerase [9014-24-8] and maintains template activity similar to that in free solution λ Plaques can be lifted onto 3MM filter disks, deproteinized, and used for transcription assays in **vitro**. The RNA synthesized is complementary to phage rather than to E. coli DNA and plaques can be identified by autoradiog. Furthermore, the filters can subsequently be probed with radioactive nucleic acids under standard hybridization conditions. Finally, colorimetric assays can be employed with lactate dehydrogenase [9001-60-9] isoenzyme A in which plaques are identified by the localized reduction of nitroblue tetrazolium.

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=> s p2A (5w)(peptide or polypeptide or protein)
          127 P2A
       273170 PEPTIDE
        86631 POLYPEPTIDE
      1411336 PROTEIN
L13           8 P2A (5W)(PEPTIDE OR POLYPEPTIDE OR PROTEIN)

=> d l13 1-8 ti au so py ab

L13  ANSWER 1 OF 8  CA  COPYRIGHT 2002 ACS
TI   Antigenic Epitopes of the Hepatitis A Virus Polyprotein
AU   Khudyakov, Yury E.; Lopareva, Elena N.; Jue, Danny L.; Fang, Sunan;
     Spelbring, John; Krawczynski, Krzysztof; Margolis, Harold S.; Fields,
     Howard A.
SO   Virology (1999), 260(2), 260-272
     CODEN: VIRLAX; ISSN: 0042-6822
PY   1999
AB   Forty-two antigenic domains were identified across the hepatitis A virus
     (HAV) polyprotein by using a set of 237 overlapping 20-mer synthetic
     peptides spanning the entire HAV polyprotein and a panel of serum samples
     from acutely HAV-infected patients. The term "antigenic domain" is used
     here to define a protein region spanned with consecutive overlapping
     immunoreactive peptides. Nineteen antigenic domains were found within
the
     structural proteins, and 22 were found within the nonstructural proteins,
     with 1 domain spanning the junction of VP1 and P2A proteins. Five of
     these domains were considered immunodominant, as judged by both the
     breadth and the strength of their immunoreactivity. One domain is
located
     within the VP2 protein at position 57-90 aa. A second domain, located at
     position 767-842 aa, contains the C-terminal part of the VP1 protein and
     the entire P2A protein. A third domain, located at
     position 1403-1456 aa, comprises the C-terminal part of the P2C protein
     and the N-terminal half of the P3A protein. The fourth domain, located
at
     position 1500-1519 aa, includes almost the entire P3B, and the last
     domain, located at position 1719-1764 aa, contains the C-terminal region
     of the P3C protein and the N-terminal region of the P3D protein. It is
     interesting to note that 4 of the 5 most immunoreactive domains are
     derived from small HAV proteins and/or encompass protein cleavage sites
     separating different HAV proteins. The HAV-specific immunoreactivity of
each
     antigenically reactive peptide was confirmed by using 7 HAV
seroconversion
     panels. Thus, HAV structural and nonstructural proteins contain
antigenic
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epitopes that can be efficiently modeled with short synthetic peptides. (c) 1999 Academic Press.

L13 ANSWER 2 OF 8 CA COPYRIGHT 2002 ACS
TI The protein kinase C inhibitor H7 blocks phosphorylation of stathmin during TPA-induced growth inhibition of human pre-B leukemia REH6 cells
AU Duraj, Jozef; Kovacikova, Maria; Sedlak, Jan; Koppel, Juraj; Sobel, Andre;
Chorvath, Branko
SO Leukemia Research (1995), 19(7), 457-61
CODEN: LEREDD; ISSN: 0145-2126
PY 1995
AB The human pre-B acute lymphoblastic leukemia cell line REH6 was used to analyze the regulation of a ubiquitous intracellular phosphoprotein stathmin (Mr 19,000, pl=5.6-6.2). We demonstrated by 32P-labeling that the short (1 h) treatment of the REH6 cells with the tumor promoting phorbol ester, 12-O-tetradecanoylphorbol-13-acetate (TPA), resulted in a rapid phosphorylation of at least three (P1, P2 and P3) stathmin isoforms without an alteration of stathmin isoform expression. Furthermore, Western blot anal. with specific antiserum showed that the prolonged period (48 h) of TPA treatment partially reduced protein levels particularly of two (N2 and P2) stathmin isoforms. The potent and relatively specific protein kinase C (PKC) inhibitor, 1,(5-isoquinolinesulfonyl)2methylpiperasine dihydrochloride (H7), partially inhibited these TPA effects, whereas the specific calmodulin inhibitor R24571 (calmidazolium) had no effect upon these events. Our findings suggest that stathmin phosphorylation in REH6 cells could be in part mediated by PKC activation.

L13 ANSWER 3 OF 8 CA COPYRIGHT 2002 ACS
TI A nucleotide sequence comparison of coxsackievirus B4 isolates from aquatic samples and clinical specimens
AU Hughes, M. S.; Hoey, E. M.; Coyle, P. V.
SO Epidemiology and Infection (1993), 110(2), 389-98
CODEN: EPINEU; ISSN: 0950-2688
PY 1993
AB Ten coxsackievirus B4 (CVB4) strains isolated from clin. and environmental
sources in Northern Ireland in 1985-7, were compared at the nucleotide sequence level. Dideoxynucleotide sequencing of a polymerase chain reaction (PCR) amplified fragment, spanning the VP1/P2A genomic region, classified the isolates into two distinct groups or genotypes as defined by Rico-Hesse and colleagues for poliovirus type 1. Isolates within each group shared approx. 99% sequence identity at the nucleotide level whereas
≤86% sequence identity was shared between groups. One isolate derived from a clin. specimen in 1987 was grouped with six CVB4 isolates recovered from the aquatic environment in 1986-7. The second group comprised CVB4 isolates from clin. specimens in 1985-6. Both groups were different at the nucleotide level from the prototype strain isolated in 1950. It was concluded that the method could be used to sub-type CVB4 isolates and would be of value in epidemiol. studies of CVB4. Predicted amino acid sequences revealed non-conservation of the tyrosine residue at the VP1/P2A cleavage site but were of little value in distinguishing CVB4 variants.

L13 ANSWER 4 OF 8 CA COPYRIGHT 2002 ACS
TI Isolation of plant virus RNA-dependent replicase and virus-resistant transgenic plants producing inhibitors of the replicase
IN Buck, Kenneth William; Hayes, Robert James

SO PCT Int. Appl., 51 pp.
CODEN: PIXXD2
PY 1992
1992
1993
AB The RNA-dependent replicase comprising cucumber mosaic virus P1a and **P2a** proteins and **protein** P50 of tobacco is isolated. Transgenic plants producing an antibody to these proteins, of antisense RNA to RNA encoding these proteins, are expected to be virus-resistant (no data). The isolated replicase catalyzed the cucumber mosaic virus-RNA-dependent synthesis of pos.-strand, as well as neg.-strand, RNA. Monoclonal antibodies to constituent proteins were produced. Some of these antibodies inhibited replicase activity. The cDNA for the tobacco P50 protein was cloned. Based on amino acid sequence similarities, the P50 protein was proposed to be β-amylase.

L13 ANSWER 5 OF 8 CA COPYRIGHT 2002 ACS
TI Requirement for ICR-like sequences in the replication of brome mosaic virus genomic RNA
AU Pogue, Gregory P.; Marsh, Loren E.; Connell, James P.; Hall, Timothy C.
SO Virology (1992), 188(2), 742-53
CODEN: VIRLAX; ISSN: 0042-6822
PY 1992
AB Previous studies using a brome mosaic virus (BMV) RNA-2 deletion mutant (pRNA-2 M/S) and addnl. derivs. as reporters established that viral sequences resembling internal control regions (ICRs) 1 and 2 of tRNA gene promoters are vital to (+)-strand replication in protoplasts. Transfer of these mutations to genomic RNA-2 and functional anal. in protoplast, local lesion, and systemic infections revealed a sequence-specific requirement for bases within the ICR2-like motif. Despite the low (generally <20% of wild-type) and sometimes undetectable levels of replication of these RNA-2 mutants, sufficient **p2a protein** was produced to support at least modest levels of RNA-1, -3 and -4 replication in protoplasts. However, only these RNA-2 ICR2 mutants supporting substantial replication of the viral genome in protoplasts were capable of establishing local lesions in Chenopodium hybridium and systemic infections in barley, further establishing the essential role of the ICR-like sequences in viral infectivity. Upon passage through a second set of barley plants, accumulation patterns for progeny from inocula containing certain RNA-2 mutants paralleled those from wild-type inocula, indicating repair of the introduced mutations. RNA stability and translatability were shown to be unaffected by the introduced mutations. BMV RNA-3 contains several ICR-like sequences, each of which was individually deleted. Whereas deletion of the 5'-terminal ICR2-like motif had little effect on RNA-3 accumulation in protoplasts or local lesion formation, it debilitated systemic spread in barley. Deletion of an internal ICR2-like motif at position 1100 decreased (+):(-) strand asymmetry from >100:1 to 14:1, reduced RNA-3 replication in protoplasts to less than 15% of wild-type, and abolished local lesion and systemic infectivity.

L13 ANSWER 6 OF 8 CA COPYRIGHT 2002 ACS

TI Non-replicating deletion mutants of brome mosaic virus RNA-2 interfere with viral replication
AU Marsh, Loren E.; Pogue, Gregory P.; Szybiak, Urzula; Connell, James P.; Hall, Timothy C.
SO Journal of General Virology (1991), 72(10), 2367-74
CODEN: JGVIAY; ISSN: 0022-1317
PY 1991
AB Naturally occurring defective interfering RNAs (DI-RNAs) and satellite RNAs greatly reduce the accumulation of their helper virus in vivo, but often modulate symptom expression in an unpredictable manner. Deletion mutants Nc/S, Na/M and Sa/Nc + M/S, derived from brome mosaic virus (BMV) RNA-2, failed to replicate when co-inoculated with BMV RNAs-1 and -2 to barley protoplasts. Owever, the inoculum RNA corresponding to these deletion mutants was extremely stable and could have been mistaken for plus-strand progeny had minus-strand progeny anal. been omitted. These results accentuate the need for such tests in evaluating the ability of mutant viral sequences to replicate. One of the mutants, Nc/S, effectively interfered with the accumulation of BMV RNas-1 and -2 in barley protoplasts. This non-replicating interfering RNA was termed NRI RNA-2 Nc/S. when present with RNAs-1 and -2 at low inoculum amts. (1 μg), NRI RNA-2 Nc/S reduced replication of RNA-2, the parental RNA, by 63% and preferentially interfered with minus-strand RNA accumulation. At higher levels (4 μg), it completely displaced replication f both RNAs-1 and -2. Mutations eliminating translation of a truncated **p2a protein** from NRI RNA-2 Nc/S did not alleviate the interference effect, demonstrating that a defective replicase protein was not responsible for the decreased accumulation of genomic RNA. At an NRI RNA:
genomic RNA inoculum molar ration of 1:1, NRI RNA-2 Nc/S reduced the accumulation of all helper virus RNAs by 55%. Since this reduction was seen
for both wild-type RNA-3 and δSGP RNA-3, a deletion mutant of RNA-3 that lacks the subgenomic promoter necessary for coat protein expression, it was evident that the effective interference mediated by NRI RNA-2 Nc/S was not mitigated by encapsidation. The ability of the NRI RNAs to mimic satellite DI RNAs in depressing helper virus replication suggests that their expression in transgenic plants may provide a new and widely applicable approach for inducing resistance to viral infection.

L13 ANSWER 7 OF 8 CA COPYRIGHT 2002 ACS
TI The effect of poliovirus proteinase 2Apro expression on cellular metabolism. Inhibition of DNA replication, RNA polymerase II transcription, and translation
AU Davies, Monique V.; Pelletier, Jerry; Meerovitch, Karen; Sonenberg, Nahum;
Kaufman, Randal J.
SO Journal of Biological Chemistry (1991), 266(22), 14714-20
CODEN: JBCHA3; ISSN: 0021-9258
PY 1991
AB Infection of cells with poliovirus results in a rapid inhibition of host RNA and protein synthesis. Concordant with this shutoff, the p220 subunit
of the cap-binding protein complex is cleaved, probably indirectly, by the
poliovirus proteinase p2A (2Apro). To elucidate the mechanism of action of 2Apro in inhibiting protein synthesis in vivo, the effect of transient expression of 2Apro in COS-1 monkey kidney cells was studied. In cells transfected with a 2Apro expression plasmid, p220 was cleaved and the 2Apro mRNA was reduced 30-fold compared to an identical plasmid containing a